

STIC-Biotech/ChemLib

129094

From: Slobodyansky, Elizabeth  
Sent: Wednesday, August 04, 2004 5:04 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/430,029

Please search for case 09/430,029:

*removed EG*

SEQ ID NO: 8 against commercial ~~and interference~~ databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652  
REM 3A65  
571-272-0941  
MAILBOX 3C70

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: *8/5/04*  
Date Completed: *8/5/04*  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: *DS*  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 5, 2004, 13:09:29 ; Search time 54 Seconds  
(without alignments)  
617.419 Million cell updates/sec

Title: US-09-430-029-8  
Perfect score: 619

Sequence: 1 MDAGRVCVTIAQTDERYA.....RLRKPFPCGACAGTAANK 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	619	100.0	118	3 AAY84822	Amino aci
2	418.5	67.6	111	3 AAY96262	R. eutrop
3	322	52.0	119	7 AAO23395	Pseudomon
4	259.5	41.9	112	4 AAG64662	Hydroxyin
5	228.5	36.9	101	2 AAW98976	Alcaligen
6	144.5	23.3	342	2 AAR66216	Nocardia
7	144.5	23.3	342	2 AAR81472	Nocardia
8	130.5	21.1	343	6 ABU22750	Protein e
9	129.5	20.9	329	2 AAW80338	Oxidase a
10	126.5	20.4	343	6 ABU21309	Protein e
11	124.5	20.1	343	6 ABU19841	Protein e
12	123	19.9	346	6 ABP97021	Sphingomo
13	123	19.9	346	6 ABP97025	Sphingomo
14	120	19.4	366	6 ABU41589	Protein e
15	117	18.9	368	6 ABU40068	Protein e
16	113	18.3	366	6 ABU38911	Protein e
17	111	17.9	405	6 ABP79217	N. gonorr
18	110	17.8	92	2 AAW14449	CarB gene
19	109.5	17.7	336	6 ABP78930	N. gonorr
20	109.5	17.7	336	6 ABU37353	Protein e
21	109	17.6	348	6 ABU22973	Protein e
22	105	17.0	350	2 AAR05385	Xylene ox
23	105	17.0	350	6 ABP97023	Pseudomon
24	104.5	16.9	326	4 AAB60228	C Glutami
25	103.5	16.7	512	4 AAG92388	

## ALIGNMENTS

RESULT 1  
AAY84822

ID AAY84822 standard; protein; 118 AA.

AC AAY84822;

DT 08-AUG-2000 (first entry)

DE Amino acid sequence of toluene monooxygenase TomQ.

KW Toluene monooxygenase; TomK; TomL; TomM; TomO; TomP; TomQ; toluene;  
KW ortho-cresol; 3-methylcatechol; chlorinated compound;  
KW aliphatic hydrocarbon; trichloroethylene; dichloroethylene; phenol;  
KW aromatic compound; benzene; cresol; environmental remediation.

OS Burkholderia cepacia.

FN EP999274-A2.

PD 10-MAY-2000.

PF 02-NOV-1999; 99EP-00121681.

PR 30-OCT-1998; 98JP-00310801.

PA (CANO ) CANON KK.

PI Yano T, Nomoto T, Imamura T;

DR WPI; 2000-306010/27.

DR N-PSDB; AAA14845.

PT Novel DNA fragment encoding a toluene monooxygenase, useful for degrading  
a chlorinated aliphatic hydrocarbon compound, or an aromatic compound,  
e.g. in environmental remediation.

PS Claim 46; Page 45; 52pp; English.

CC AAY84816-22 represent toluene monooxygenase enzymes TomK, TomL, TomM,  
TomN, TomO, TomP, and TomQ, respectively. The enzymes oxidise toluene to  
ortho-cresol and 3-methylcatechol. The toluene monooxygenase has a high  
efficiency in degrading aromatic and volatile organic chlorinated  
compounds. The nucleic acids are useful for the recombinant production of  
toluene monooxygenase. Toluene monooxygenase is useful for degrading a  
chlorinated aliphatic hydrocarbon compound (e.g. trichloroethylene (TCE)  
or dichloroethylene (DCE)), or an aromatic compound (e.g. toluene,  
benzene, phenol, and cresol), e.g. in environmental remediation. It is  
especially useful for purifying air polluted with chlorinated aliphatic

Abu40855 Protein e  
Abu29472 Burkholde  
Abu21907 Protein e  
Abu38023 Protein e  
Abu25632 Protein e  
Abu61631 Protein e  
Abu20107 Protein e  
Abu78834 N. gonorr  
Abu50056 Protein e  
Ada35088 Acinetoba  
Abu31645 Protein e  
Abu21203 Protein e  
Abu48037 Protein e  
Aay35534 Chlamydia  
Abu27042 Protein e  
Abu2741 Protein e  
Abu15018 Protein e  
Aau23193 Novel hum  
Aay96261 R. eutrop  
Aaw98975 Alcaligen

26 103 16.6 334 6 ABU40855  
27 103 16.6 342 3 AAB29472  
28 103 16.6 419 6 ABU21907  
29 101.5 16.4 336 6 ABU38023  
30 101 16.3 664 6 ABU25632  
31 100.5 16.2 348 6 ABR61631  
32 100 16.2 382 6 ABU20107  
33 99.5 16.1 96 6 ABP78834  
34 99 16.0 340 6 ABU50056  
35 96 15.5 358 6 ADA35088  
36 92.5 14.9 322 6 ABU31645  
37 92.5 14.9 345 6 ABU21203  
38 91.5 14.8 323 6 ABU48037  
39 90.5 14.6 431 2 AAY35534  
40 90.5 14.6 431 6 ABU27042  
41 90 14.5 381 6 ABU2741  
42 89.5 14.5 322 6 ABU15018  
43 89.5 14.5 336 4 AAU23193  
44 88 14.2 352 3 AAY96261  
45 88 14.2 356 2 AAW98975





Thu Aug 5 15:10:14 2004

us-09-430-029-8.rag

XX PS Claim 2; Page 4-5; 30pp; Japanese.

XX CC E.coli transformed with the DNA sequence AAQ79569 are able to catalyze

XX CC the epoxidation of alkenes. The DNA is derived from Nocardia corallina

XX CC and comprises 4 open reading frames. ORFs amoA and amoC encode subunits 1

XX CC and 2 of the alkene monooxygenase enzyme and ORF amoD encodes a reductase

XX CC capable of transferring electrons from NADH coenzyme to a monooxygenase.

XX CC (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 342 AA;

Query Match 23.3%; Score 144.5; DB 2; Length 342;

Best Local Similarity 38.6%; Pred. No. 4.6e-08;

Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;

QY 9 TTTTAQTDERYACVSGESLLAGMAKLGRRGIPVGLNGGCGVKRVLRGAVRKLGPISR 68

Db 3 TINQPSHESYSCDEGESLLDG-ALRNSLLKYGCKHGCGTCKVRLDGDVEEPGS-SF 60

QY 69 AHVSAEENDGYALACRVVP--DGDVELEVAGRLRKPFGC 107

Db 61 ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEEFFSG 100

RESULT 7

AA81472

ID AAR81472 standard; protein; 342 AA.

AC AAR81472;

XX 16-OCT-2003 (revised)

DT 07-AUG-1996 (first entry)

DE Nocardia corallina alkene mono-oxygenase gene product, amoD.

XX Alkene mono-oxygenase; indole; indigo production; biosynthesis;

KW microbial oxidation; dye.

OS Gordonia rubripertinctus; B-276.

XX JP08023988-A.

PD 30-JAN-1996.

XX 08-JUL-1994; 94JP-00179688.

PF 08-JUL-1994; 94JP-00179688.

XX (NIHA ) JAPAN ENERGY CORP.

PA WPI; 1996-133426/14.

DR N-PSDB; AAT17418.

XX Prepn. of indigo by a microbiological method - by culturing a microbe

PT having alkene monooxygenase activity to oxidise indole to indigo.

XX Claim 5; Page 8-9; 11pp; Japanese.

XX AAR81469-R81472 are protein products of the Nocardia corallina strain B-

XX 276 alkene mono-oxygenase gene. The gene encodes 4 protein products amoA,

XX amoB, amoC and amoD derived from the 3 different reading frames of the

XX operon. The gene is useful for the production of indigo via oxidation of

XX indole. Nocardia corallina can be cultured in a medium contg. indole and

XX will readily oxidise the indole yielding indigo into the culture medium.

XX E. coli may also be transformed with the alkene mono-oxygenase gene and

XX used as above to efficiently produce indigo by microbial oxidation.

XX (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 342 AA;

Query Match 23.3%; Score 144.5; DB 2; Length 342;

Best Local Similarity 38.6%; Pred. No. 4.6e-08;

Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;

QY 9 TTTTAQTDERYACVSGESLLAGMAKLGRRGIPVGLNGGCGVKRVLRGAVRKLGPISR 68

Db 3 TINQPSHESYSCDEGESLLDG-ALRNSLLKYGCKHGCGTCKVRLDGDVEEPGS-SF 60

QY 69 AHVSAEENDGYALACRVVP--DGDVELEVAGRLRKPFGC 107

Db 61 ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEEFFSG 100

RESULT 8

ABU22750

ID ABU22750 standard; protein; 343 AA.

XX AC ABU22750;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #8277.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia mallei.

XX WO200277183-A2.

XX 03-OCT-2002.

PD 21-MAR-2002; 2002WO-US009107.

PF 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA26620.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 50674; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid

XX encoding a polypeptide whose expression is inhibited by the antisense

XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the

XX antisense nucleic acid; (4) an antibody capable of specifically binding

XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for

XX proliferation; (7) identifying a compound that influences the activity of

XX the gene product or that has an activity against a biological pathway

XX required for proliferation, or that inhibits cellular proliferation; (8)

XX identifying a gene required for cellular proliferation or the biological

XX pathway in which a proliferation-required gene or its gene product lies

XX on a gene on which the test compound that inhibits proliferation of an

XX organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX compound's activity; (11) a culture comprising strains in which the gene

XX product is overexpressed or underexpressed; (12) determining the extent

XX to which each of the strains is present in a culture or collection of

XX strains; or (13) identifying the target of a compound that inhibits the

XX proliferation of an organism. The antisense nucleic acids are useful for









isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 69513; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 366 AA;

Query Match 19.4%; Score 120; DB 6; Length 366;  
Best Local Similarity 37.2%; Pred. No. 3.4e-05;  
Matches 32; Conservative 9; Mismatches 41; Indels 4; Gaps 2;

QY 10 VTIAQDERYACVSGESLLAGMAKLGRRGIPVGLNGGCGVKVRVLRGAVRKLGPISRA 69  
Db 284 VFETDTGKSIKRVAPGETVHAAAKVGLM-IPKACGMGICGTCVKMLSGEVEM--EHNG 339  
QY 70 HVSABEENDGYALACRVVDPGDVELE 95  
Db 340 GTTDEDVARGYILSCSVKPGDVRIE 365

RESULT 15  
ABU40068  
ID ABU40068 standard; protein; 368 AA.  
XX ABU40068;  
AC ABU40068;  
XX 19-JUN-2003 (first entry)  
DT DE Protein encoded by Prokaryotic essential gene #25595.  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Pseudomonas putida.  
OS WO200277183-A2.  
PN 03-OCT-2002.  
PD 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR

25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPT; 2003-029926/02.  
DR N-PSDB; ACA43938.  
XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 67992; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 368 AA;

Query Match 18.9%; Score 117; DB 6; Length 368;  
Best Local Similarity 40.3%; Pred. No. 7.6e-05;  
Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

QY 24 GESLLAGMAKLGRRGIPVGLNGGCGVKVRVLRGAVRKLGPISRAHVSABEENDGYALA 83  
Db 300 GETVHAAAKVGLM-IPKACGMGICGTCVKMLSGEVEM--EHNGGITEDEAGYILS 355  
QY 84 CRVVPDGDVELE 95  
Db 356 CCSVPRKGDVRID 367

Search completed: August 5, 2004, 13:15:40  
Job time : 57 secs



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; FILE REFERENCE: BC1016 US NA
; CURRENT APPLICATION NUMBER: US/09/716,865
; CURRENT FILING DATE: 2000-11-26
; PRIOR APPLICATION NUMBER: 60/167,062
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Pseudomonas CT14
US-09-716-865-2

Query Match          52.0%; Score 322; DB 4; Length 119;
Best Local Similarity 56.4%; Pred. No. 7e-31;
Matches 62; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY      9  TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGCGVCVKVRVLRGAVRKLGPISR 68
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      10  SVHVMTGTETPCATDESLLQGMLRLGRKGIPGVGVNCGGCVCVKVHVEGQCRLPGPVS 69
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      69  AHVSAEENDGYALACRVDPDGDVELEVAGRRLKPFFCGMACAGTAANK 118
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      70  AHVSAABEARGFTLACKVAEVTPVQLEWVGKFEKVFSKFVSTNEIINK 119
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 3
US-08-499-215-5
; Sequence 5, Application US/08499215
; Patent No. 5612204
; GENERAL INFORMATION:
; APPLICANT: Saeki, Hisashi
; APPLICANT: Miura, Akira
; TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
; TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: N.W.
; STATE: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatenIn Release #1.0, Version #1.30
; SOFTWARE: & WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,215
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP Hei-6-179689
; FILING DATE: 08-JUL-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-499-215-5

Query Match          23.3%; Score 144.5; DB 1; Length 342;
Best Local Similarity 38.6%; Pred. No. 4.1e-09;
Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;

QY      9  TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGCGVCVKVRVLRGAVRKLGPISR 68
DB      3  TINVPFSEHYSCSDPSLLDG-AARNLSLLKYCKGGCGCTCKVRLDGDVBEFGS-SF 60
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      69  AHVSAEENDGYALACRVDP--DGDVELEVAGRRLKPFFCG 107
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```

US-08-737-825-7
; Sequence 7, Application US/08737825
; Patent No. 5871922
; GENERAL INFORMATION:
; APPLICANT: SALMOND, GEORGE PEACOCK COPELAND
; APPLICANT: MCGOWAN, SIMON JAMES
; APPLICANT: SEBAHIA, MOHAMMED
; APPLICANT: COX, ANTHONY RICHARD JOHN
; APPLICANT: HOLDEN, MATTHEW THOMAS GEOFFREY
; APPLICANT: PORTER, LAUREN ELIZABETH
; APPLICANT: BYCROFT, BARRIE WALSHAM
; APPLICANT: WILLIAMS, PAUL
; APPLICANT: STEWART, GORDON SIDNEY ANDERSON BIRNIE
; TITLE OF INVENTION: GENES INVOLVED IN THE BIOSYNTHETIC PATHWAY OF CARBAPENEM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,825
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1009-0105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Erwinia carotovora

US-08-737-825-7
Query Match 17.8%; Score 110; DB 2; Length 92;
Best Local Similarity 39.7%; Pred. No. 1e-05;
Matches 29; Conservative 11; Mismatches 25; Indels 8; Gaps 3;

QY 25 ESSLAGMAKLRGRRGIPVGLNGCGGVCKVRLGAVR--KLGPISSRAHVAEENDGYAL 82
Db 21 ESVLSAYEAGVE-LPYRCASGYGVCKVRLTSGNVNMDHSGGISRKDIA-----DGYIL 74

QY 83 ACRVVPDGDVLE 95
Db 75 PCCSVPLSNLEIE 87

RESULT 7
5171684-7
; Patent No. 5171684
; APPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R.
; TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
; MONOOXYGENASE OF PSEUDOMANAS MENDOCINA KR-1
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/590,374

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; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 177,631
; FILING DATE: 05-APR-1988
; SEQ ID NO: 7:
; LENGTH: 326
; 5171684-7

Query Match 16.9%; Score 104.5; DB 6; Length 326;
Best Local Similarity 31.5%; Pred. No. 0.00023;
Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 14 QDDE---RYACVSGESLLAGMAKLRGRRGIPVGLNGCGGVCKVRLGAVRKLGPISRAH 70
Db 5 QSDLLHFEADNSDTLLSA-ALRAELVFFYECNCGCGACKTELLEGEVSNLWP-DAPG 62

QY 71 VSAEEENDGYALACRVVPDGDVLEVAGR 99
Db 63 LAARELKNRFLACQCKPLSLDKIKVINR 91

RESULT 8
US-09-543-681A-7190
; Sequence 7190, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7190
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7190

Query Match 16.6%; Score 103; DB 4; Length 353;
Best Local Similarity 34.1%; Pred. No. 0.00038;
Matches 30; Conservative 13; Mismatches 37; Indels 8; Gaps 3;

QY 9 TVTIAQTDERYACVSGESLLAGMAKLRGRRGIPV--GCLNGCGGVCKVRLGAVRKLGP 66
Db 271 TWTIRHPLKQINVPVGMWILLTAMEE---NSVPVLAACRAGVCGSCKTRIVKGDYE---VT 324

QY 67 SRAHVAEENDGYALACRVVPDGDVLE 94
Db 325 STSTLTADRIAQGYVLACSCRLTGDVLE 352

RESULT 9
US-09-328-352-6375
; Sequence 6375, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6375
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6375

Query Match 15.5%; Score 96; DB 4; Length 358;

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Best Local Similarity 30.9%; Pred. No. 0.0026;  
 Matches 25; Conservative 12; Mismatches 32; Indels 12; Gaps 3;  
 QY 10 VTTAQTDERVACVSGESLLAGMAKLGRRGIPVGCGLNGCGVCKVRLRGAVRKLGPISRA 69  
 Db 281 VSVAQDD-----ESILDAALRAG-ADLPYACKGGVCAFCCKVL-SGEYDMFLNYS-- 329  
 QY 70 HVSAAEENDGYALACRVVDPDG 90  
 Db 330 -LEEDEVEKGYVLSQTLIPKG 349

RESULT 10  
 US-09-543-681A-5480  
 ; Sequence 5480, Application US/09543681A  
 ; Patent No. 6605709  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GARY BRETON  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709.1002-001  
 ; CURRENT APPLICATION NUMBER: US/09/543.681A  
 ; CURRENT FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/128,706  
 ; PRIOR FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 8344  
 ; SEQ ID NO 5480  
 ; LENGTH: 411  
 ; TYPE: PRT  
 ; ORGANISM: Proteus mirabilis  
 US-09-543-681A-5480

Query Match 15.3%; Score 94.5; DB 4; Length 411;  
 Best Local Similarity 32.1%; Pred. No. 0.0047;  
 Matches 27; Conservative 17; Mismatches 33; Indels 7; Gaps 4;  
 QY 16 DERVACVSGESLLAGMAKLGRRGIPV--GCLNGG-CGVCKVRLRGAVRKLGPISRAHVS 72  
 Db 47 EKSFPAGDKL---NVLSNEGIFISSACGGGCGQCKVKVLEGGGDL-PTLSHIN 102  
 QY 73 ABEENDGYALACRVVDPGDVELEV 96  
 Db 103 KREAKEGCRACQVNVKNLKL 126

RESULT 11  
 US-09-489-039A-12074  
 ; Sequence 12074, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489.039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 12074  
 ; LENGTH: 339  
 ; TYPE: PRT  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-12074

Query Match 14.9%; Score 92.5; DB 4; Length 339;  
 Best Local Similarity 35.9%; Pred. No. 0.0064;  
 Matches 28; Conservative 10; Mismatches 35; Indels 5; Gaps 3;  
 QY 17 BRYACVSGESLLAGMAKLGRRGIPVGCGLNGCGVCKVRLRGAVRKLGPISRAHVSAREE 76  
 Db 266 EBYAPV-GTLLDAL-ESNKVPTVACRAGVCGGCKTKVSG---KYSVTMTLITDAEI 320

QY 77 NDGYALACRVVDPGDVEL 94  
 Db 321 ADGVVLACSCHPQSDVL 338  
 RESULT 12  
 US-09-489-039A-9429  
 ; Sequence 9429, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489.039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 9429  
 ; LENGTH: 377  
 ; TYPE: PRT  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-9429  
 Query Match 14.7%; Score 91; DB 4; Length 377;  
 Best Local Similarity 29.7%; Pred. No. 0.011;  
 Matches 27; Conservative 17; Mismatches 43; Indels 4; Gaps 3;  
 QY 9 TTTTAAQTDERVACVSGESLLAGMAKLGRRGIPVGCGLNGCGVCKVRLRGAVRKLGPIS 67  
 Db 290 TITLASTGERWP-VPGDKTIAQVLQEHGVAVPLSCMGICGACLTTPVREGTVDRHRTVQS 348  
 QY 68 RAHVSAREENDGYALACRVVDPGDVELEVAG 98  
 Db 349 EAEQAAEQH--IALCCRSLSANLIVIDLAG 377

RESULT 13  
 US-09-198-452A-952  
 ; Sequence 952, Application US/09198452A  
 ; Patent No. 6559294  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Griffiths, R.  
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
 ; TITLE OF INVENTION: and treatment of infection  
 ; FILE REFERENCE: 9710-003-999  
 ; CURRENT APPLICATION NUMBER: US/09/198.452A  
 ; CURRENT FILING DATE: 1998-11-24  
 ; NUMBER OF SEQ ID NOS: 6849  
 ; SEQ ID NO 952  
 ; LENGTH: 431  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia pneumoniae  
 US-09-198-452A-952

Query Match 14.6%; Score 90.5; DB 4; Length 431;  
 Best Local Similarity 32.5%; Pred. No. 0.015;  
 Matches 26; Conservative 14; Mismatches 33; Indels 7; Gaps 3;  
 QY 23 SGESLLAGMAKLGRRGIPVGCGLNGG---CGVCKVRLRGAVRKLGPISRAHVSAREENDG 79  
 Db 57 SGQTLVLSLS--SGIPSPCGGKATCKQCKVVRVKNNADEPL-ETDRSTFSKRQLEEG 112  
 QY 80 YALACRVVDPGDVELEVAGR 99  
 Db 113 WRLSCQCKVQHDMSLEIBER 132

RESULT 14  
 US-09-453-956-7  
 ; Sequence 7, Application US/09453956

```

; Patent No. 6472191
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya; No. 6472191oto, Tsuyoshi; Imamura, Takeshi;
; APPLICANT: Canon Kabushiki Kaisha
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
; TITLE OF INVENTION: Method for Degrading Halogenated Aliphatic Hydrocarbon
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and
; TITLE OF INVENTION: Method for Environmental Remediation
; FILE REFERENCE: CP014074US
; CURRENT APPLICATION NUMBER: US/09/453,956
; CURRENT FILING DATE: 1999-12-03
; EARLIER APPLICATION NUMBER: JP P1998-344506
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Ralstonia eutropha
; FEATURE:
; OTHER INFORMATION: Tomp polypeptide
US-09-453-956-7

Query Match      14.2%; Score 88; DB 4; Length 352;
Best Local Similarity 34.7%; Pred. No. 0.023;
Matches 25; Conservative 9; Mismatches 36; Indels 2; Gaps 2;

QY 24 GESILAGMAKLRGIRIPVCLNGCGVCKVRVLGAVRKLGPIGRAHVSAEEENDGYALA 83
Db 19 GQTILDAALQGIIY-IPHACCHGLCGTCKVSLDGEA-DLGEANPFALMDFEREGKALA 76
QY 84 CRVVPDGDVELE 95
Db 77 CCATLQADTTIE 88

RESULT 15
US-09-489-039A-12111
; Sequence 12111, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12111
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12111

Query Match      14.2%; Score 88; DB 4; Length 381;
Best Local Similarity 31.2%; Pred. No. 0.026;
Matches 25; Conservative 14; Mismatches 33; Indels 8; Gaps 3;

QY 9 TVTIAQTDERYACVSGESILAGMAKLRGIRIPVCLNGCGVCKVRVLGAVRKLGPIGR 68
Db 302 TVALEWQGGQFTNNQOVLEQEQGIR-VPYSCRAGICGSCRIRLEGEV---SPLKK 357
QY 69 AHVSAEEENDGYALACRVVP 88
Db 358 NAVA-----GDGTLACSCVP 373

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Job time : 19 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 5, 2004, 13:08:34 ; Search time 46 Seconds  
(without alignments)  
804.665 Million cell updates/sec

Title: US-09-430-029-8

Perfect score: 619

Sequence: 1 MDAGRVCVTITAOQTDERYA.....RLKPFPCGMACGTAANK 118

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Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	619	100.0	118	9	US-09-430-029-8
2	418.5	67.6	111	14	US-10-223-371B-8
3	130.5	21.1	343	12	US-10-282-122A-50674
4	126.5	20.4	343	12	US-10-282-122A-49233
5	124.5	20.1	343	12	US-10-282-122A-47765
6	123	19.9	346	14	US-10-213-878-12
7	123	19.9	346	14	US-10-213-878-22
8	123	19.9	346	14	US-10-214-059-12
9	123	19.9	346	14	US-10-214-059-22
10	120	19.4	366	12	US-10-282-122A-69513
11	117	18.9	368	12	US-10-282-122A-67992
12	113	18.3	366	12	US-10-282-122A-66835
13	109.5	17.7	336	12	US-10-282-122A-65277
14	109	17.6	348	12	US-10-282-122A-50897
15	105.5	17.0	169	12	US-10-424-599-275773

16	105	17.0	350	14	US-10-213-878-18	Sequence 18, Appl
17	105	17.0	350	14	US-10-214-059-18	Sequence 18, Appl
18	103.5	16.7	186	12	US-10-425-114-47415	Sequence 47415, A
19	103.5	16.7	512	9	US-09-738-626-6142	Sequence 6142, Ap
20	103	16.6	334	12	US-10-282-122A-68779	Sequence 68779, A
21	103	16.6	419	12	US-10-282-122A-49831	Sequence 49831, A
22	101.5	16.4	336	12	US-10-282-122A-65947	Sequence 65947, A
23	101	16.3	664	12	US-10-282-122A-53556	Sequence 53556, A
24	100	16.2	382	12	US-10-282-122A-48031	Sequence 48031, A
25	99	16.0	340	12	US-10-282-122A-77980	Sequence 77980, A
26	94.5	15.3	354	14	US-10-156-761-11884	Sequence 11884, A
27	92.5	14.9	322	12	US-10-282-122A-59569	Sequence 59569, A
28	92.5	14.9	345	12	US-10-282-122A-49127	Sequence 49127, A
29	91.5	14.8	323	12	US-10-282-122A-75961	Sequence 75961, A
30	90.5	14.6	431	12	US-10-282-122A-54966	Sequence 54966, A
31	90.5	14.6	431	15	US-10-289-762-952	Sequence 952, App
32	90	14.5	381	12	US-10-282-122A-50665	Sequence 50665, A
33	89.5	14.5	322	12	US-10-282-122A-42942	Sequence 42942, A
34	89	14.4	145	12	US-10-424-599-150076	Sequence 150076, A
35	88	14.2	352	14	US-10-223-371B-7	Sequence 7, Appli
36	87	14.1	322	12	US-10-282-122A-55785	Sequence 55785, A
37	86.5	14.0	431	12	US-10-282-122A-55074	Sequence 55074, A
38	84.5	13.7	83	16	US-10-437-963-133198	Sequence 133198, A
39	84.5	13.7	322	12	US-10-282-122A-66811	Sequence 66811, A
40	82	13.2	322	12	US-10-282-122A-69345	Sequence 69345, A
41	81	13.1	354	9	US-09-430-029-7	Sequence 7, Appli
42	80.5	13.0	134	15	US-10-216-464-31	Sequence 31, Appl
43	79.5	12.8	338	12	US-10-282-122A-44836	Sequence 44836, A
44	78.5	12.7	152	12	US-10-425-114-66819	Sequence 66819, A
45	78.5	12.7	152	12	US-10-425-114-67176	Sequence 67176, A

#### ALIGNMENTS

##### RESULT 1

US-09-430-029-8  
; Sequence 8, Application US/094300029  
; Patent No. US20020168738A1  
; GENERAL INFORMATION:

; APPLICANT: Yano, Tetsuya; No. US20020168738A1oto, tsuyoshi; Imamura, Takeshi; Canon I  
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,  
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,  
; TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon  
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and  
; TITLE OF INVENTION: Method for Environmental Remediation  
; FILE REFERENCE: CF013982US  
; CURRENT APPLICATION NUMBER: US/09/430,029  
; CURRENT FILING DATE: 1999-10-29  
; EARLIER APPLICATION NUMBER: JP P1998-310801  
; EARLIER FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Burkholderia cepacia  
; FEATURE:  
; OTHER INFORMATION: TomQ polypeptide

US-09-430-029-8

Query Match 100.0%; Score 619; DB 9; Length 118;

Best Local Similarity 100.0%; Pred. No. 6.8e-64;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAGRVCVTITAOQTDERYACVSGSLLAGMAKLRGRGIPVGLNGCGVCVKVRVLRGAV 60

Db 1 MDAGRVCVTITAOQTDERYACVSGSLLAGMAKLRGRGIPVGLNGCGVCVKVRVLRGAV 60

QY 61 RLKGFPTSAHVSAAEENDGYALACRVDPDGVLEVAGRLRKPFCGMACGTAANK 118

Db 61 RLKGFPTSAHVSAAEENDGYALACRVDPDGVLEVAGRLRKPFCGMACGTAANK 118

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RESULT 2
US-10-223-371B-8
; Sequence 8, Application US/10223371B
; Publication No. US20030170877A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya; No. US20030170877A1oto, Tsuyoshi; Imamura, Takeshi; Canon
; APPLICANT: Kabushiki Kaisha
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene, Recombinant
; TITLE OF INVENTION: Plasmid, Transformed Microorganism, Method for Degrading Halogen
; TITLE OF INVENTION: Aliphatic Hydrocarbon Compounds and Aromatic Compounds, and Meth
; TITLE OF INVENTION: Environmental Remediation
; FILE REFERENCE: 03500.014074.1
; CURRENT APPLICATION NUMBER: US/10/223.371B
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US/09/453.956
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 8
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Ralstonia eutropha
; FEATURE:
; OTHER INFORMATION: TomQ polypeptide
US-10-223-371B-8

Query Match 67.6%; Score 418.5; DB 14; Length 111;
Best Local Similarity 76.7%; Pred. No. 1.2e-40;
Matches 79; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY 9 TTTAQTDERVACVSGESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISR 68
Db 8 TVRVAQTGESFSCSTAGESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISR 67

QY 69 AHVSAEEENDGYALACRVVPGDVELEVAGRLRKPFFCGMACA 111
Db 68 AHVSADEEGLYTLACRVAPQGDVELEVAGRWKQKFLC--CA 107

RESULT 3
US-10-282-122A-50674
; Sequence 50674, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

Query Match 21.1%; Score 130.5; DB 12; Length 343;
Best Local Similarity 33.7%; Pred. No. 1.5e-06;
Matches 31; Conservative 19; Mismatches 37; Indels 5; Gaps 3;

QY 10 VTIACQDERVACVSGESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISR 69
Db 5 VTLKQSGRQFQVEADETVLAALRNQVH-LPYGCKNGACGCKGTIVOGQFEQ-GPHSAS 62

QY 70 HVSAAEENDGYALACRVVPGDVEL---EVAG 98
Db 63 ALSNDRTRGLALLCCSKPQSDLEVDVREIAG 94

RESULT 4
US-10-282-122A-49233
; Sequence 49233, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 49233
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49233

Query Match      20.4%; Score 126.5; DB 12; Length 343;
Best Local Similarity 35.4%; Pred. No. 4.4e-06;
Matches 34; Conservative 15; Mismatches 34; Indels 13; Gaps 4;

QY 10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISRA 69
Db 5 VTLKQSGRQFQVEQDEPVLAAALRQVH-IPYCKNGAGCSCKGTIVISGEIEQ-----RA 58
QY 70 H-----VSAEENDGYALACRVVDPGDVEL-----EVAG 98
Db 59 HSSALSNEEKTRGMALFCCATCTDLEVDIREVAG 94

RESULT 5
US-10-282-122A-47765
; Sequence 47765, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITEA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47765
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-282-122A-47765

Query Match      20.1%; Score 124.5; DB 12; Length 343;
Best Local Similarity 32.6%; Pred. No. 7.5e-06;
Matches 30; Conservative 20; Mismatches 37; Indels 5; Gaps 3;
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QY 10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISRA 69
Db 5 VTLKQSGRQFQVEQDEPVLAAALRQVH-IPYCKNGAGCSCKGTIVISGEIEQ-GPHAAS 62
QY 70 HVSAAEENDGYALACRVVDPGDVEL-----EVAG 98
Db 63 ALSNDERTRGLALLCCSKAQCDLEIDVREIAG 94

RESULT 6
US-10-213-878-12
; Sequence 12, Application US/10213878
; Publication No. US20030073206A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; APPLICANT: Nagarajan, Vasantha
; APPLICANT: Thomas, Stuart
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
; FILE REFERENCE: CL1662 US NA
; CURRENT APPLICATION NUMBER: US/10/213,878
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Sphingomonas sp.
US-10-213-878-12

Query Match      19.9%; Score 123; DB 14; Length 346;
Best Local Similarity 30.1%; Pred. No. 1.1e-05;
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

QY 9 TTVIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISR 68
Db 12 TVTVEGSPITLDIPAGKTLLEMLDAG-LAMPDCKVSGCTCKFKLVSKIGELSPSAL 70
QY 69 AHVSAEENDGYALACRVVDPGDVELEVAGRLKPKFFCGMACA 111
Db 71 A-LEGDELSRGLACQAIIPRDLTIAVDA---PLSQGIAIA 108

RESULT 7
US-10-213-878-22
; Sequence 22, Application US/10213878
; Publication No. US20030073206A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; APPLICANT: Nagarajan, Vasantha
; APPLICANT: Thomas, Stuart
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
; FILE REFERENCE: CL1662 US NA
; CURRENT APPLICATION NUMBER: US/10/213,878
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Sphingomonas sp.
US-10-213-878-22

Query Match      19.9%; Score 123; DB 14; Length 346;
Best Local Similarity 30.1%; Pred. No. 1.1e-05;
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

QY 9 TTVIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISR 68
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Db 12 TTVTVEGPTTLDIPAGKTLLEAMLDAG-LAMPHDCKVSGCGTKFKLVSGKIGELSPSAL 70  
QY 69 AHVSAEENDGYALACRVVDPDGVLELVAGRLKRPFFCGMACA 111  
Db 71 A-LEGDELSRGFLACQAI PRSDLTIAVDA----PLSQGIAIA 108

RESULT 8  
US-10-214-059-12  
; Sequence 12, Application US/10214059  
; Publication No. US20030077768A1  
; GENERAL INFORMATION:  
; APPLICANT: Bramucci, Michael  
; APPLICANT: Nagarajan, Vasantha  
; APPLICANT: Thomas, Stuart  
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted Polycyclic Aromatic Compounds  
; FILE REFERENCE: CL1663 US NA  
; CURRENT APPLICATION NUMBER: US/10/214,059  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 60/311,486  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 12  
; LENGTH: 346  
; TYPE: PRT  
; ORGANISM: Sphingomonas sp.  
US-10-214-059-12

Query Match 19.9%; Score 123; DB 14; Length 346;  
Best Local Similarity 30.1%; Pred. No. 1.1e-05;  
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;  
QY 9 TTVTIAQTDERYACVSGESILLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR 68  
Db 12 TTVTVEGPTTLDIPAGKTLLEAMLDAG-LAMPHDCKVSGCGTKFKLVSGKIGELSPSAL 70  
QY 69 AHVSAEENDGYALACRVVDPDGVLELVAGRLKRPFFCGMACA 111  
Db 71 A-LEGDELSRGFLACQAI PRSDLTIAVDA----PLSQGIAIA 108

RESULT 9  
US-10-214-059-22  
; Sequence 22, Application US/10214059  
; Publication No. US20030077768A1  
; GENERAL INFORMATION:  
; APPLICANT: Bramucci, Michael  
; APPLICANT: Nagarajan, Vasantha  
; APPLICANT: Thomas, Stuart  
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted Polycyclic Aromatic Compounds  
; FILE REFERENCE: CL1663 US NA  
; CURRENT APPLICATION NUMBER: US/10/214,059  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 60/311,486  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 22  
; LENGTH: 346  
; TYPE: PRT  
; ORGANISM: Sphingomonas sp.  
US-10-214-059-22

Query Match 19.9%; Score 123; DB 14; Length 346;  
Best Local Similarity 30.1%; Pred. No. 1.1e-05;  
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;  
QY 9 TTVTIAQTDERYACVSGESILLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR 68

Db 12 TTVTVEGPTTLDIPAGKTLLEAMLDAG-LAMPHDCKVSGCGTKFKLVSGKIGELSPSAL 70  
QY 69 AHVSAEENDGYALACRVVDPDGVLELVAGRLKRPFFCGMACA 111  
Db 71 A-LEGDELSRGFLACQAI PRSDLTIAVDA----PLSQGIAIA 108

RESULT 10  
US-10-282-122A-69513  
; Sequence 69513, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 69513  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Pseudomonas syringae  
US-10-282-122A-69513

Query Match 19.4%; Score 120; DB 12; Length 366;  
Best Local Similarity 37.2%; Pred. No. 2.7e-05;  
Matches 32; Conservative 9; Mismatches 41; Indels 4; Gaps 2;  
QY 10 VTIAQTDERYACVSGESILLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR 69  
Db 284 VFTDTGKSIRVAPGETVHAAAAGLGLM-IPKACGAGICGTCKWKLSGVEVM---EHNG 339

RESULT 11  
US-10-282-122A-67992  
; Sequence 67992, Application US/10282122A

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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67992
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-67992

Query Match      18.9%; Score 117; DB 12; Length 368;
Best Local Similarity 40.3%; Pred. No. 6,1e-05;
Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

QY 24 GESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISRAHVSAEENDGYALA 83
Db 300 GETVHAARAAKVLGLM-IPKACGMGICGTCKVLKLGVEVEM---EHNHGITEDEAGYILS 355
QY 84 CRVVPDGDVELE 95
Db 356 CCSVPKGDVRID 367

RESULT 12
US-10-282-122A-66835
; Sequence 66835, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

```

```

; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66835
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66835

Query Match      18.3%; Score 113; DB 12; Length 366;
Best Local Similarity 37.3%; Pred. No. 0.00018;
Matches 28; Conservative 12; Mismatches 25; Indels 10; Gaps 3;

QY 24 GESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISRAH---VSAEENDGY 80
Db 298 GETVHAARAAKVLGLH-IPKACGMGICGTCKV-----MKTAGEVEMEHNGITDEDVAEGY 350
QY 81 ALACRVVPDGDVELE 95
Db 351 ILSCCSVPKGDVVVID 365

RESULT 13
US-10-282-122A-65277
; Sequence 65277, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21

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1  RESULT 14
2  US-10-282-122A-50897
3  Sequence 50897, Application US/10282122A
4  Publication No. US20040029129A1
5  GENERAL INFORMATION:
6  APPLICANT: Wang, Liangsu
7  APPLICANT: Zamudio, Carlos
8  APPLICANT: Malone, Cheryl
9  APPLICANT: Haselbeck, Robert
10 APPLICANT: Ohlsen, Kari
11 APPLICANT: Zyskind, Judith
12 APPLICANT: Wall, Daniel
13 APPLICANT: Trawick, John
14 APPLICANT: Carr, Grant
15 APPLICANT: Yamamoto, Robert
16 APPLICANT: Forsyth, R.
17 APPLICANT: Xu, H.
18 TITLE OF INVENTION: Identification of E
19 FILE REFERENCE: ELITRA.034A
20 CURRENT APPLICATION NUMBER: US/10/282,1
21 CURRENT FILING DATE: 2003-02-20
22 PRIOR APPLICATION NUMBER: 60/191,078
23 PRIOR FILING DATE: 2000-03-21
24 PRIOR APPLICATION NUMBER: 60/206,948
25 PRIOR FILING DATE: 2000-05-23
26 PRIOR APPLICATION NUMBER: 60/207,727
27 PRIOR FILING DATE: 2000-05-26
28 PRIOR APPLICATION NUMBER: 60/230,335
29 PRIOR FILING DATE: 2000-09-06
30 PRIOR APPLICATION NUMBER: 60/230,347
31 PRIOR FILING DATE: 2000-09-09
32 PRIOR APPLICATION NUMBER: 60/242,578
33 PRIOR FILING DATE: 2000-10-23

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[illegible]

Search completed: August 5, 2004, 13:14:34  
Job time : 48 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 5, 2004, 13:13:39 ; Search time 16 Seconds  
(without alignments)  
709.413 Million cell updates/sec

Title: US-09-430-029-8  
Perfect score: 619  
Sequence: 1 MDAGRVCTVITIAQTDERYA.....RLRKPFFCCMACAGTAINK 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195.5	31.6	112	1 S16193	ferredoxin [2Fe-2S]
2	186	30.0	108	1 B39181	ferredoxin [2Fe-2S]
3	172.5	27.9	93	2 T31266	ferredoxin [2Fe-2S]
4	172.5	27.9	112	1 S24417	ferredoxin [2Fe-2S]
5	166.5	26.9	101	1 S54762	ferredoxin [2Fe-2S]
6	129.5	20.9	329	2 T46585	ferredoxin [2Fe-2S]
7	123	19.9	346	2 T31263	ferredoxin reducta
8	114	18.4	337	2 A12723	xylene monooxygena
9	114	18.4	337	2 E97505	naphthalene 1,2-di
10	113	18.3	366	2 G82970	phenol hydroxylase
11	112	18.1	411	1 D64052	probable ferredoxi
12	106	17.1	353	2 A95312	Na+-translocating
13	105	17.0	350	2 B37316	probable dioxigena
14	104.5	16.9	326	1 A47016	ferredoxin-NAD red
15	104	16.8	405	2 D81918	ferredoxin [2Fe-2S]
16	104	16.8	405	2 G81184	toluene-4-monooxyg
17	102	16.5	369	2 AG0825	sodium-translocati
18	101.5	16.4	181	2 A86451	Na(+)-translocatin
19	101.5	16.4	336	2 F81849	conserved hypothet
20	101	16.3	378	2 AF3320	probable ferredoxi
21	100.5	16.2	348	1 JQ0701	probable CDP-6-deo
22	99.5	16.1	122	2 S75687	Flavohemoprotein [
23	99	16.0	340	2 A10165	methane monooxygen
24	99	16.0	408	2 B82094	probable oxidoredu
25	99	16.0	685	2 C70878	sodium-translocati
26	98	15.8	353	1 S44308	probable electron
27	98	15.8	353	2 F37831	phenol 2-monooxyge
28	98	15.8	354	2 C95381	probable oxidoredu
29	98	15.8	407	1 S65531	sodium-translocati

## ALIGNMENTS

## RESULT 1

S16193 ferredoxin [2Fe-2S]-like protein xylT - Pseudomonas putida plasmid pW00

C:Species: Pseudomonas putida  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: S16193; S23486  
R:Harayama, S.; Polissi, A.; Rekik, M.

FEBS Lett. 285, 85-88, 1991

A:Title: Divergent evolution of chloroplast-type ferredoxins.

A:Reference number: S16193; MUID:91293320; PMID:2065785

A:Accession: S16193

A:Molecule type: DNA

A:Residues: 1-112 <HAR>

A:Cross-references: EMBL:X61467; MID:g311898; PIDN:CAA43702.1; PID:g311899

R:Neidle, E.L.; Hartnett, C.; Orntson, L.N.; Bairoch, A.; Rekik, M.; Harayama, S.

Eur. J. Biochem. 204, 113-120, 1992

A:Title: Cis-diol dehydrogenases encoded by the TOL pW00 plasmid xylT gene and the Acine

A:Reference number: S23477; MUID:92155191; PMID:1740120

A:Accession: S23486

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-112 <NEI>

A:Cross-references: EMBL:M64747; MID:g151718; PIDN:AA26051.1; PID:g151723

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992

C:Genetics:

A:Gene: xylT

A:Genome: plasmid pW00

C:Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology

C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein

F;25-82/Domain: ferredoxin [2Fe-2S] homology <FER>

F;41,46,49,81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 31.6%; Score 195.5; DB 1; Length 112;

Best Local Similarity 48.1%; Pred. No. 3.4e-12;

Matches 38; Conservative 13; Mismatches 27; Indels 1; Gaps 1;

QY 17 ERVACVSGSLLAGMAKLGRIIPVCLNGGCGVKRVLRGAVRKLGPISRHHVSAEE 76

Db 15 QSFRCAGGQSVLRAMEAQGRKCIIPVCGRGCGCLCRVRLSGAYRS-GRMSRGHVPKAA 73

QY 77 NDGYALACRWPDGDVELE 95

Db 74 AEALACQVFFQTDLTIE 92

## RESULT 2

B39181

ferredoxin [2Fe-2S]-like protein nahG-nahH intergenic region - Pseudomonas putida (stra

C:Species: Pseudomonas putida

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: B39181; S16368

R:You, I.S.; Ghosal, D.; Gunsalus, I.C.

Biochemistry 30, 1635-1641, 1991  
A;Title: Nucleotide sequence analysis of the Pseudomonas putida PpG7 salicylate hydroxylase  
A;Reference number: A39181; MUID:91129237; PMID:1993181  
A;Accession: B39181  
A;Molecule type: DNA  
A;Residues: 1-108 <YOU>  
A;Cross-references: GB:M60055; GB:J05317; NID:g151380; PIDN:AAA35898.1; PID:g151382  
R;Harayama, S.; Polissi, A.; Reik, M.  
FEBS Lett. 285, 85-88, 1991  
A;Title: Divergent evolution of chloroplast-type ferredoxins.  
A;Reference number: S16193; MUID:91293320; PMID:2065785  
A;Accession: S16368  
A;Molecule type: DNA  
A;Residues: 1-108 <HAR>  
A;Cross-references: GB:X61466; GB:S40145; NID:g311896; PIDN:CAA43701.1; PID:g311897  
C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology  
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein  
F;24-81/Domain: ferredoxin [2Fe-2S] homology <FER>  
F;40.45/48.80/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted  
A;Accession: S16368  
Query Match 30.0%; Score 186; DB 1; Length 108;  
Best Local Similarity 42.6%; Pred. No. 2.8e-11;  
Matches 40; Conservative 12; Mismatches 38; Indels 4; Gaps 2;  
QY 10 VTIAGTDYACVSGESLLAGMAKLGRRGIPVGLNGCGCKVRLGAVRKLGPISKA 69  
DB 7 ITVQPGGRFVCPQPOQSALHMETQKRCPLVCGRGCGCKVRLAGDYES-GRVSK 65  
QY 70 HVSAREENDGVALACRVVDPDGDVELEVAGRLRP 103  
DB 66 HLFVARECGVALACRLFARSCLIE--RYSKP 96  
RESULT 3  
T31266  
ferredoxin [2Fe-2S]-like protein xylT - Sphingomonas aromaticivorans plasmid pNL1  
C;Species: Sphingomonas aromaticivorans  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G  
submitted to the EMBL Data Library, July 1998  
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati  
A;Reference number: Z20392  
A;Accession: T31266  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-93 <ROM>  
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378407; PIDN:AA03990.1  
C;Genetics:  
A;Gene: xylT  
A;Genome: plasmid pNL1  
Query Match 27.9%; Score 172.5; DB 2; Length 93;  
Best Local Similarity 44.3%; Pred. No. 5.1e-10;  
Matches 35; Conservative 12; Mismatches 31; Indels 1; Gaps 1;  
QY 18 RVACVSGESLLAGMAKLGRRGIPVGLNGCGCKVRLGAVRKLGPISRAHVSAAEEN 77  
DB 15 QFACPEGERVLLIAMESGGNDIGVCGRGCGCFVVRVGEYR-TGKMSTAKVSAADQA 73  
QY 78 DGYALACRVVDPDGDVELEV 96  
DB 74 KGYVALACRLPLNDLVIEI 92  
RESULT 4  
S24417  
ferredoxin [2Fe-2S]-like protein dmpQ - Pseudomonas putida  
C;Species: Pseudomonas putida  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C;Accession: S24417  
R;Shingler, V.; Powlowski, J.; Marklund, U.  
J. Bacteriol. 174, 711-724, 1992

A;Title: Nucleotide sequence and functional analysis of the complete phenol/3,4-dimethy  
A;Reference number: S24417; MUID:92121108; PMID:1732207  
A;Accession: S24417  
A;Molecule type: DNA  
A;Residues: 1-112 <SHI>  
A;Cross-references: EMBL:X60657; NID:g45687; PIDN:CAA43064.1; PID:g45688  
C;Genetics:  
A;Gene: dmpQ  
C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology  
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein  
F;25-82/Domain: ferredoxin [2Fe-2S] homology <FER>  
F;41.46/49.81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted  
Query Match 27.9%; Score 172.5; DB 1; Length 112;  
Best Local Similarity 41.0%; Pred. No. 6.1e-10;  
Matches 34; Conservative 16; Mismatches 32; Indels 1; Gaps 1;  
QY 17 ERYACVSGESLLAGMAKLGRRGIPVGLNGCGCKVRLGAVRKLGPISRAHVSAAEE 76  
DB 15 QTFRCPLDQSVLSAMEQKRCVFPVCGRGCGCKVRLSGTY-QCHKMSCHNHPPEAA 73  
QY 77 NDGYALACRVVDPDGDVELEVAGR 99  
DB 74 QOGLALACQLPQTDNLIECLR 96  
RESULT 5  
S24762  
ferredoxin [2Fe-2S]-like protein phlG - Pseudomonas putida  
C;Species: Pseudomonas putida  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C;Accession: S24762; B58972; S44309; S47420  
R;Hermann, H.; Mueller, C.; Schmidt, I.; Mahne, J.; Petruschka, L.; Hahnke, K.  
Mol. Gen. Genet. 247, 240-246, 1995  
A;Title: Localization and organization of phenol degradation genes of Pseudomonas putida  
A;Reference number: S24761; MUID:95272534; PMID:7753034  
A;Accession: S24762  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-101 <HER>  
A;Cross-references: EMBL:X80765; NID:g527546; PIDN:CAA56746.1; PID:g527553  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
R;Ng, L.C.; Shingler, V.; Sze, C.C.; Poh, C.L.  
Gene 151, 29-36, 1994  
A;Title: Cloning and sequences of the first eight genes of the chromosomally encoded  
A;Reference number: A58972; MUID:95129877; PMID:7828892  
A;Accession: B58972  
A;Molecule type: DNA  
A;Residues: 1-72, 'GB', '75-101 <NGL>  
A;Cross-references: EMBL:X79063; NID:g483477; PIDN:CAA55666.1; PID:g483484  
A;Experimental source: strain P35X (NCBI 9869)  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994  
C;Genetics:  
A;Gene: phlG  
C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology  
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein  
F;25-82/Domain: ferredoxin [2Fe-2S] homology <FER>  
F;41.46/49.81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted  
Query Match 26.9%; Score 166.5; DB 1; Length 101;  
Best Local Similarity 40.0%; Pred. No. 2.2e-09;  
Matches 34; Conservative 17; Mismatches 33; Indels 1; Gaps 1;  
QY 17 ERYACVSGESLLAGMAKLGRRGIPVGLNGCGCKVRLGAVRKLGPISRAHVSAAEE 76  
DB 15 QSTFCRDPDQSVLRAMEEQKRCVFPVCGRGCGCKVRLSGDY-QCGRMSCSQVPEAA 73  
QY 77 NDGYALACRVVDPDGDVELEVAGRLR 101  
DB 74 QOGLALACQLYPRADLYIESLRQVR 98  
RESULT 6



T46585  
ferredoxin reductase [imported] - Pseudomonas stutzeri  
C:Species: Pseudomonas stutzeri  
C>Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 11-May-2000  
C:Accession: T46585  
R:Ouchiyaama, N.; Miyachi, S.; Omori, T.  
J. Gen. Appl. Microbiol. 44, 57-63, 1998  
A:Title: Cloning and nucleotide sequence of carbazole catabolic genes from Pseudomonas  
A:Reference number: 223091  
A:Accession: T46585  
A:Status: preliminary  
A:Map position: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-329 <OUC>  
A:Cross-references: EMBL:AB001723; PIDN:BAA31273.1  
A:Experimental source: strain OM1  
C:Function:  
A:Description: involved in carbazole degradation [validated, PIR:223091]  
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog

Query Match 20.9%; Score 129.5; DB 2; Length 329;  
Best Local Similarity 39.0%; Pred. No. 2.9e-05;  
Matches 30; Conservative 11; Mismatches 35; Indels 1; Gaps 1;  
QY 21 CVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISRAHVSAAEENDGY 80  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
14 CGSGKSLVLSALANG-IGFPVECASGCGVCKFELLSGNVQSMWPDAGLSRRDREKGNR 72  
QY 81 ALACRVVDPGDVELEVA 97  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
73 HLACQCVALSRLRIKVA 89

RESULT 7  
T31263  
xylene monooxygenase (EC 1.-.-.-) chain A - Sphingomonas aromaticivorans plasmid pNL1  
C:Species: Sphingomonas aromaticivorans  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C:Accession: T31263  
R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G  
submitted to the EMBL Data Library, July 1998  
A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati  
A:Reference number: 220992  
A:Accession: T31263  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-346 <ROM>  
A:Cross-references: EMBL:AF079317; NID:G3378261; PID:G3378404; PIDN:AAD03987.1  
C:Genetics:  
A:Gene: xylA  
A:Genome: plasmid pNL1  
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog  
C:Keywords: oxidoreductase

Query Match 19.9%; Score 123; DB 2; Length 346;  
Best Local Similarity 30.1%; Pred. No. 0.00013;  
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;  
QY 9 TWTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISR 68  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
12 TTVTEGSPPTLLDIPAGTKTLLLEMLDAG-LAMPHDCKVSGCTCKFKLVSGKIGELSPSAL 70  
QY 69 AHVSAEEENDGYALACRVVDPGDVELEVAAGRLRKPFCGMACA 111  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
71 A-LEGDELRSGRFLACQAIPTSLDTTAVDA---PLSQGIATA 108

RESULT 8  
AI2723  
naphthalene 1,2-dioxygenase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AI2723  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AI2723  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-337 <KUR>  
A:Cross-references: GB:AE008688; PIDN:AAL42207.1; PID:gl7739599; GSPDB:GN00186  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atul196  
A:Map position: circular chromosome  
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog  
C:Keywords: 2Fe-2S; metalloprotein  
F:40,45,48,80/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 18.4%; Score 114; DB 2; Length 337;  
Best Local Similarity 33.3%; Pred. No. 0.00098;  
Matches 31; Conservative 13; Mismatches 33; Indels 16; Gaps 4;  
QY 9 TWTIAQTDERYACVSGESLL-----AGMAKLGRRGIPVGCINGCGVCKVRLRGAV--R 61  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
7 TTYLPQIGRSIMAAEGETVLAALAGIA-----YPRGCRMGRCGACKSHLISGEIDLL 60  
QY 62 KLGPISRAHVSAAEENDGYALACRVVDPGDVEL 94  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
61 KHTPFS---LTBEKAEGLTLACRAVPASDVTI 90

RESULT 9  
E97505  
phenol hydroxylase component, poXF (AF026065) [imported] - Agrobacterium tumefaciens (st  
C:Species: Agrobacterium tumefaciens  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: E97505  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: E97505  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-337 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK86998.1; PID:gl5156240; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C 2205  
A:Map position: circular chromosome  
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog  
C:Keywords: 2Fe-2S; metalloprotein  
F:40,45,48,80/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 18.4%; Score 114; DB 2; Length 337;  
Best Local Similarity 33.3%; Pred. No. 0.00098;  
Matches 31; Conservative 13; Mismatches 33; Indels 16; Gaps 4;  
QY 9 TWTIAQTDERYACVSGESLL-----AGMAKLGRRGIPVGCINGCGVCKVRLRGAV--R 61  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
7 TTYLPQIGRSIMAAEGETVLAALAGIA-----YPRGCRMGRCGACKSHLISGEIDLL 60  
QY 62 KLGPISRAHVSAAEENDGYALACRVVDPGDVEL 94  
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
61 KHTPFS---LTBEKAEGLTLACRAVPASDVTI 90

RESULT 10  
GB2970  
probable ferredoxin P45411 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa

```
A95312
probable dioxxygenase reductase subunit [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
```

A;Genome: plasmid pWWO

C:Function:  
A:Description: catalyzes hydroxylation of a methyl side-chain of toluene and xylenes;  
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homo  
C:Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; FAD; flavoprotein; heterodimer; i  
F:37-93/Domain: ferredoxin [2Fe-2S] homology <FER>  
F:121-344/Domain: cytochrome-b5 reductase homology <CBR>  
F:152-57 60 92/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

```
Query Match      17.0%; Score 105; DB 2; Length 350;
Best Local Similarity 28.4%; Pred. No. 0.0078;
Matches 25; Conservative 18; Mismatches 43; Indels 2; Gaps 2;

QY 9 TTVTAQTDERVACVSGESLLAGMAKLGRRGIPVGLNGCGVCKVRVLRGAVRKLGPISR 68
Db 19 TVSVRGQGFQFKVPRGQTILESALHGG-IAFPHDCKVSGCGTKYKLIISGRNEL-TSSA 76
QY 69 AHVSAEEENDGYALACRVVPGDVELEV 96
Db 77 MGLSGDLYQSGYRLGCGCQIPKEDLEIEL 104

RESULT 14
A47016
toluene-4-monooxygenase (EC 1.-.-.-) reductase component - Pseudomonas mendocina
C:Species: Pseudomonas mendocina
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A47016
R:Yen, K.M.; Karl, M.R.
J. Bacteriol. 174, 7253-7261, 1992
A:Title: Identification of a new gene, tmoF, in the Pseudomonas mendocina KRI gene cluster
A:Reference number: A47016; MUID:93054339; PMID:1429451
A:Accession: A47016
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <YEN>
A:Cross-references: GB:M95045; NID:gl51596; PIDN:AAA26004.1; PID:gl51597
A:Experimental source: KRI
A>Note: sequence extracted from NCBI backbone (NCBIN:118027, NCBIP:118029)
C:Genetics:
A:Gene: tmoF
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
C:Keywords: 2Fe-2S; flavoprotein; iron-sulfur protein; metalloprotein; oxidoreductase
F:21-77/Domain: ferredoxin [2Fe-2S] homology <FER>
F:107-320/Domain: cytochrome-b5 reductase homology <CBR>
F:36,41,44,76/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match      16.9%; Score 104.5; DB 1; Length 326;
Best Local Similarity 31.5%; Pred. No. 0.0082;
Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 14 QTDE---RYACVSGESLLAGMAKLGRRGIPVGLNGCGVCKVRVLRGAVRKLGPISRAH 70
Db 5 QSDDLLHFFEADSDNTLLSA-ALRAELVFPYCNSGCGACKIELLEGEVSNLWP-DAPG 62
QY 71 VSAEEENDGYALACRVVPGDVELEVAGR 99
Db 63 LAARELKNRFLACQCKPLSLKIKVINR 91

RESULT 15
D81918
sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) chain F NMA0747 [simil]
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: D81918
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: D81918
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84030.1; PID:g737946
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: nqrF; NMA0747
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
C:Keywords: NAD; oxidoreductase
```

```
Query Match      16.8%; Score 104; DB 2; Length 405;
Best Local Similarity 35.2%; Pred. No. 0.011;
Matches 32; Conservative 14; Mismatches 41; Indels 4; Gaps 4;

QY 8 GTVTIAQTDERVACV-SGESLLAGMAKLGRRGIPVGLNGG-CGVCKVRVLRGAVRKLGP 65
Db 32 GDITIKVNGEKELTMPAGGKLIGALANEG-IFIPSA CGGSGCGCRVVVKSGGGDIL-P 89
QY 66 ISRAHVSAAEEENDGYALACRVVPGDVELEV 96
Db 90 TELSHISKREAREGRLSCQNVNKTMDIEV 120
```

Search completed: August 5, 2004, 13:17:20  
Job time : 17 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 5, 2004, 13:09:59 ; Search time 13 Seconds  
(without alignments)  
472.637 Million cell updates/sec

Title: US-09-430-029-8  
Perfect score: 619  
Sequence: 1 MDAGRVCGTIVTAQTDERYA.....RLRKPFEGMACACTAANK 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	195.5	31.6	112	1	FERX_PSEPU	P23103 pseudomonas
2	186	30.0	108	1	FERN_PSEPU	P23263 pseudomonas
3	112	18.1	411	1	NQRF_HAEIN	O05012 haemophilus
4	105	17.0	350	1	XYLA_PSEPU	P21394 pseudomonas
5	104.5	16.9	326	1	TMOF_PSEME	Q03304 pseudomonas
6	104	16.8	405	1	NQRF_NEIMA	Q9JYQ3 neisseria m
7	104	16.8	405	1	NQRF_NEIMA	Q9K0M8 neisseria m
8	100.5	16.2	348	1	NQRF_PASMU	P22868 methylococc
9	100	16.2	407	1	NQRF_PASMU	Q9C1A6 pasteurella
10	99	16.0	408	1	NQRF_VIBCH	Q9X4G8 vibrio chol
11	98	15.8	352	1	DMPP_PSESP	P19734 pseudomonas
12	98	15.8	407	1	NQRF_VIBAL	Q56584 v na(+)-tra
13	96	15.5	407	1	NQRF_VIBPA	Q9L6J0 vibrio para
14	96	15.5	407	1	NQRF_VIBVU	Q8DBJ1 vibrio vuln
15	93	15.0	407	1	NQRF_YERPE	Q8ZBZ5 yersinia pe
16	92.5	14.9	301	1	NQRF_YERPE	Q9L6J0 vibrio vuln
17	92	14.9	93	1	FER_PSEPU	Q9L6J0 vibrio vuln
18	91	14.7	104	1	FER2_SYNBP	P19770 peridinium
19	90.5	14.6	95	1	FER_GLEJA	P08451 synchococc
20	90.5	14.6	356	1	PAAE_ECOLI	P02033 gleichenia
21	90.5	14.6	431	1	NQRF_CHLNP	P76081 escherichia
22	90	14.5	407	1	NQRF_VIBHA	Q9Z723 chlamydia p
23	89.5	14.5	96	1	FER1_PHYAM	Q9RFV6 vibrio harv
24	89.5	14.5	96	1	FER1_PHYES	P00229 phytolacca
25	89.5	14.5	303	1	NQRF_COLMA	Q9K3E1 colwellia m
26	89.5	14.5	303	1	NQRF_VIBPS	Q9L6J2 vibrio psyc
27	89.5	14.5	322	1	HCR_ECOLI	P75924 escherichia
28	88.5	14.3	431	1	NQRF_CHLTR	O84745 chlamydia t
29	88	14.2	328	1	NDOR_PSEPU	Q52126 pseudomonas
30	87.5	14.1	348	1	BENC_ACICA	P07771 acinetobact
31	87	14.1	93	1	FER2_EQUITE	P00236 equisetum t
32	86.5	14.0	431	1	NQRF_CHLMU	Q9PLI3 chlamydia m
33	86	13.9	93	1	FER2_EQUAR	P00237 equisetum a

34	85.5	13.8	303	1	NORF_ALTHA	Q9L6J4 alteromonas
35	85.5	13.8	431	1	NORF_CHLCV	Q821Q3 chlamydophi
36	84.5	13.7	97	1	FER1_APHEL	P00244 aphanizomen
37	84.5	13.7	148	1	FER_ARATH	P16972 arabidopsis
38	84.5	13.7	303	1	NORF_PHOPO	Q9L6J1 photobacter
39	84	13.6	148	1	FER2_ARATH	O04090 arabidopsis
40	83.5	13.5	146	1	FER_SILPR	P04669 silene prat
41	83	13.4	907	1	MOP_DESGI	Q46509 desulfovibr
42	81.5	13.2	352	1	DMPP_ACICA	Q7W6J2 acinetobact
43	81	13.1	97	1	FER_SAMNI	P00226 sambucus ni
44	81	13.1	369	1	YCBX_ECOLI	P75863 escherichia
45	80.5	13.0	96	1	FER1_SYNBP	P31965 synchococc

## ALIGNMENTS

RESULT 1  
FERX\_PSEPU  
ID FERN\_PSEPU STANDARD; PRT; 112 AA.  
AC P23103;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ferredoxin, plant-type.  
GN XYLT.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP MEDLINE=91293320; PubMed=2065785;  
RX Harayama S., Polissi A., Reik M.;  
RA "Divergent evolution of chloroplast-type ferredoxins.";  
RT FEBS Lett. 285:85-88(1991).  
RL CC  
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer electrons in a wide variety of metabolic reactions.  
CC -!- PATHWAY: Catechol metabolism.  
CC -!- SIMILARITY: Belongs to the 2Fe2S plant-type ferredoxin family.  
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CC EMBL; X61467; CAA43702.1; -;  
CC EMBL; M64747; AAA26051.1; -;  
CC PIR; S16193; S16193.  
CC InterPro; IPR006058; 2Fe2S\_fd\_BS.  
CC InterPro; IPR001041; Ferredoxin.  
CC Pfam; PF00111; fer2; 1.  
CC PROSITE; PS00197; 2Fe2S\_FERREDOXIN; 1.  
CC Aromatic hydrocarbons catabolism; Electron transport; Metal-binding;  
KW Iron-sulfur; Iron; 2Fe-2S; Plasmid.  
FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 46 46 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 49 49 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 81 81 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
SQ SEQUENCE 112 AA; 12034 MW; 799D4F03DF05D86 CRC64;

Query Match 31.6%; Score 195.5; DB 1; Length 112;  
Best Local Similarity 48.1%; Pred. No. 8.1e-13;  
Matches 38; Conservative 13; Mismatches 27; Indels 1; Gaps 1;  
QY 17 ERYACVSGESLLAGMAKLGRRGIPVGLNGGGVCKVRLGAVKLGIPISRAHVSABEE 76  
DB 15 QSFRCAGQGVLRAMEAQQKRCIPVGCRRGGCGLCRVRVLSGAVRS-GRMSRGHVPKAA 73

QY 77 NDGYALACRVVDPGDVELE 95  
: |||:| | : : |  
Db 74 AEALALACQVFPQDTLTIE 92

## RESULT 2

	FERN_PSEPU	STANDARD;	PRT;   108 AA.
ID	_FERN_PSEPU		
AC	P23263;		
DT	01-NOV-1991 (Rel. 20, Created)		
DT	01-NOV-1991 (Rel. 20, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Ferredoxin, plant-type.		
GN	NAHT.		
OS	Pseudomonas putida.		
OG	Plasmid NAH7.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
OX	NCBI TaxID=303;		

[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=G7 / ATCC 17485;  
RC MEDLINE=9129320; PubMed=2065785;  
RX Harayama S., Polissi A., Reik M.;  
RY "Divergent evolution of chloroplast-type ferredoxins.";  
RT FEBS Lett. 285:85-88(1991).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=G7 / ATCC 17485;  
RC MEDLINE=91129237; PubMed=1993181;  
RX You I.-S., Ghosal D., Gunsalus I.C.;  
RY "Nucleotide sequence analysis of the *Pseudomonas putida* PpG7  
RT salicylate hydroxylase gene (*nahG*) and its 3'-flanking region.";  
RL Biochemistry 30:1635-1641(1991).  
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer  
CC electrons in a wide variety of metabolic reactions.  
CC -!- PATHWAY: Catechol metabolism.  
CC -!- SIMILARITY: Belongs to the 2Fe2S plant-type ferredoxin family.  
CC -----  
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EMBL; X61466; CAA43701.1; -.  
DR EMBL; M60055; AAA25998.1; -.  
DR PIR; B39181; B39181.  
DR InterPro; IPR006058; 2Fe2S fd BS.  
DR InterPro; IPR001041; Ferredoxin.  
DR Pfam; PF00111; fer2; 1.  
DR PROSITE; PS00197; 2FE2S\_FERREDOXIN; 1.  
DR Aromatic hydrocarbons catabolism; Electron transport; Metal-binding;  
KW  
KW Iron-sulfur; iron; 2Fe-2S; Plasmid.  
FT METAL 40 40 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 45 45 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 48 48 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 80 80 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 80 80 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
SO SEQUENCE 108 AA: 11913 MW: 97B8181EB3361574E CRC64;

Query Match 30.0%; Score 186; DB 1; Length 108;  
Best Local Similarity 42.6%; Pred. No. 7e-12;  
Matches 40; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

Qy 10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGLNGGCGCKVRVLRGAVRKLGPISRA 69

Dd 7 ITWPGGERFVCPQQSALHMETQGKRLPVGCRGGGCLCKVRVLADYES-GRVSCK 65

QY  
70 HVSAEEENDGYALACRWVDPGDVELEVAGRLRKP 103

d6  
66 HLPVAREOGYALACELFARSDLCTIE---RYSKP 96

### RESULT 3

NQRF	HAEIN
ID	NQRF_HAEIN STANDARD; PRT; 411 AA.
AC	O05012;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, last sequence update)
DT	28-FEB-2003 (Rel. 41, last annotation update)
DE	Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE	(Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE	subunit F) (NQR-1 subunit F).
DE	NORF OR HI0171.
GN	Haemophilus influenzae.
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Haemophilus.
OX	NCBI_TaxID=727;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Rd / KW20 / ATCC 51907;
RC	MEDLINE=95350630; PubMed=7542800;
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA	McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
RA	Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA	Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.G., Smith H.O.,
RA	Venter J.C.;
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae
RT	Rd.";
RL	Science 269:496-512(1995).
RN	[2]
RP	IDENTIFICATION AS NQR SYSTEM.
RC	STRAIN=Rg / KW20 / ATCC 51907;
RC	MEDLINE=96176316; PubMed=8601449 ;
RA	Hayashi M., Nakayama Y., Unemoto T.;
RA	"Existence of Na <sup>+</sup> -translocating NADH-quinone reductase in Haemophilus
RT	influenzae".
RT	FEBS Lett. 381:174-176(1996).
RL	FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
CC	ubiquinol by two successive reactions, coupled with the transport
CC	of Na <sup>+</sup> ions from the cytoplasm to the periplasm. The first step
CC	is catalyzed by nqrF, which accepts electrons from NADH and
CC	reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer
CC	pathway.
CC	CATALYTIC ACTIVITY: NADH + ubiquinone + Na <sup>+</sup> (In) = NAD <sup>+</sup> +
CC	ubiquinol + Na <sup>+</sup> (Out).
CC	COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
CC	SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
CC	and nqrF (By similarity).
CC	SUBCELLULAR LOCATION: Inner membrane (Potential).
CC	SIMILARITY: Belongs to the nqrF family.
CC	-----
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CC	ation between the Swiss Institute of Bioinformatics and the EMBL Outstat-
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U32702; AAC21841.1; -.
DR	PIR; D64052; D64052.
DR	HSP; P23486; 1QFJ.
DR	TIGR; HI0171; -.
DR	HMAP; MF_00430; --; 1.
DR	InterPro; IPR006058; 2Fe2S_fd_BS.
DR	InterPro; IPR008333; FAD_binding_6.
DR	InterPro; IPR001041; Ferredoxin.
DR	InterPro; IPR001709; FFN cyt redctse.
DR	InterPro; IPR001433; Oxred FAD/NAD(P).

```
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PRINTS; PR00371; FENCR.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 5 27 POTENTIAL..
FT DOMAIN 38 120 FERREDOXIN..
FT DOMAIN 276 393 CATALYTIC.
FT METAL 73 73 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 82 82 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 114 114 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 411 AA; 45705 MW; E5560053E66D23E0 CRC64;

Query Match 18.1%; Score 112; DB 1; Length 411;
Best Local Similarity 34.7%; Pred. No. 0.00064;
Matches 33; Conservative 16; Mismatches 36; Indels 10; Gaps 5;

QY 8 GTVTIAQTDERYACV---SGESILAGMAKLGRRGIPV--GCLNGG-GGVCKVRVLRGAVR 61
Db 36 GDIIDINDPEKAITLPAGKLLGALAS---KGIFVSSACGGGSCGQCIVKVGKGGE 92
QY 62 KLGPISRAHSAEENDGYALACRVVDPGDVELEV 96
Db 93 IL-PTLESHINKREKGYRLACOVNVKGNNEVEL 126

RESULT 4
XYLA_PSEPU STANDARD; PRT; 350 AA.
ID XYLA_PSEPU STANDARD; PRT; 350 AA.
AC P21394;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Xylene monooxygenase electron transfer component [Includes:
DE Ferredoxin; Ferredoxin--NAD(+) reductase (EC 1.18.1.3)].
GN XYLA.
OS Pseudomonas putida.
OG Plasmid TOL pMW0.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 6-16.
RX MEDLINE=91154124; PubMed=199388;
RA Suzuki M., Hayakawa T., Shaw J.P., Rekik M., Hayayama S.;
RT "Primary structure of xylene monooxygenase: similarities to and
RT differences from the alkane hydroxylation system.";
RL J. Bacteriol. 173:1690-1695 (1991).
CC -!- FUNCTION: OXIDIZES TOLUENE AND XYLENES TO (METHYL) BENZYL
CC ALCOHOLS. THE ENZYME HAS A BROAD SPECIFICITY AND ALSO OXIDIZES
CC (METHYL) BENZYL ALCOHOLS TO (METHYL) BENZALDEHYDES AND INDOLE TO
CC INDOXYL.
CC -!- CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
CC ferredoxin + NADH.
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: COMPOSED OF TWO SUBUNITS: XYLA AND XYLM.
CC -!- SIMILARITY: IN THE N-TERMINAL REGION WITH 2FE-2S FERREDOXINS, AND
CC IN THE REST OF THE SEQUENCE WITH FERREDOXIN REDUCTASE.
CC -!- SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE
CC ELECTRON TRANSFER COMPONENTS.
CC -----
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DR EMBL; M37480; AAA26027.1; -.
DR EMBL; D63341; BAA09663.1; -.
DR PIR; B37316; B37316.
DR HSSP; P06543; 1CZP.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008333; FAD binding_6.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001709; FPN cyt reductse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR InterPro; IPR001221; Phe_hydroxylase.
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00371; FENCR.
DR PRINTS; PR00410; PHEHYDRXLASE.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; 1.
KW Aromatic hydrocarbons catabolism; Flavoprotein; Oxidoreductase; FAD;
KW NAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S; Plasmid.
FT DOMAIN 41 108 FERREDOXIN
FT METAL 109 350 FERREDOXIN-NADH REDUCTASE.
FT METAL 52 52 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 57 57 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 60 60 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 92 92 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 350 AA; 38455 MW; 26828AC2226C1DDD CRC64;

Query Match 17.0%; Score 105; DB 1; Length 350;
Best Local Similarity 28.4%; Pred. No. 0.0027;
Matches 25; Conservative 18; Mismatches 43; Indels 2; Gaps 2;

QY 9 TVTIAQTDERYACVSGESILAGMAKLGRRGIPVGCCLNGGCGVKVRVLRGAVRKLGPISR 68
Db 19 TVSVRGQGFQKVPGRQTILLESALHQG--TAPPHDCKVSGCGTKYLIISRVNEL-TSSA 76
QY 69 AHVSAEENDGYALACRVVDPGDVELEV 96
Db 77 MGLSGDLYQSGYRLGCQCIPKEDLETEL 104

RESULT 5
TMOF_PSEME STANDARD; PRT; 326 AA.
ID TMOF_PSEME STANDARD; PRT; 326 AA.
AC Q03304;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toluene-4-monooxygenase electron transfer component [Includes:
DE Ferredoxin; Ferredoxin--NAD(+) reductase (EC 1.18.1.3)].
GN TMOF.
OS Pseudomonas mendocina.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=300;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-14.
RC STRAIN=KRL;
RX MEDLINE=93054339; PubMed=1429451;
RA Yen K.-M., Karl M.R.;
RT "Identification of a new gene, tmoF, in the Pseudomonas mendocina KRL
RT gene cluster encoding toluene-4-monooxygenase.";
RL J. Bacteriol. 174:7253-7261 (1992).
CC -!- FUNCTION: ELECTRON TRANSFER COMPONENT OF TOLUENE 4-MONOOXYGENASE
CC COMPLEX.
CC -!- CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
CC ferredoxin + NADH.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: Toluene degradation; first step.
CC -!- SUBUNIT: THE MULTICOMPONENT ENZYME TOLUENE-4-MONOOXYGENASE
CC IS FORMED BY THE TMOA, TMOB, TMOG, TMOH, TMOI, TMOJ AND TMOF
CC POLYPEPTIDES.
CC -!- SIMILARITY: IN THE N-TERMINAL REGION WITH 2FE-2S FERREDOXINS, AND
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IN THE REST OF THE SEQUENCE WITH FERREDOXIN REDUCTASE.

-1- SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE ELECTRON TRANSFER COMPONENTS.

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EMBL; M95045; AAA26004.1; --  
PIR; A47016; A47016.  
InterPro; IPR006058; 2Fe2S fd BS.  
InterPro; IPR008333; FAD binding\_6.  
InterPro; IPR001041; Ferredoxin\_6.  
InterPro; IPR001709; FPN\_cyt\_redtse.  
InterPro; IPR001433; Oxred\_FAD/NAD(P).  
InterPro; IPR001221; Phe\_hydroxylase.  
Pfam; PF00970; FAD binding\_6; 1.  
Pfam; PF00111; fer2; 1.  
PRINTS; PR00371; FENCR.  
PRINTS; PR00410; PHEHYDRLASE.  
PROSITE; PS00197; 2FE2S FERREDOXIN; 1.  
KW Aromatic hydrocarbons catabolism; Flavoprotein; FAD; NAD; Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.  
FT DOMAIN 25 94 FERREDOXIN.  
FT DOMAIN 95 326  
FT METAL 36 36 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 44 44 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
SQ SEQUENCE 326 AA; 35983 MW; 17889D794FC092EE CRC64;

Query Match 16.9%; Score 104.5; DB 1; Length 326;  
Best Local Similarity 31.5%; Pred. No. 0.0029;  
Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 14 QTDE---RYCVSGESILGMAKLGRRGIPVGLNGGCGVKVRVLRGAVRKLGPISRAH 70  
Db 5 QSDLLHFEADNSNTLLSA-ALRAELVFPFCNCGGCGACKIELLEGEVSNLWP-DAPG 62

QY 71 VSAEENDGYALACRVDPDGDVELEVAGR 99  
Db 63 LAARELKNRPLACQCKPLSLDKIKVINR 91

RESULT 6

NORF NEIMA  
ID NORF NEIMA STANDARD; PRT; 405 AA.  
AC Q9JYQ3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)  
DE Na(+)-translocating NOR subunit F) (Na(+)-NOR subunit F) (NOR complex subunit F) (NOR-1 subunit F).  
GN NORF OR NMA0747.  
OS Neisseria meningitidis (serogroup A).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=65699;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;  
RX MEDLINE=20222556; PubMed=10761919;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;  
"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491";  
NATURE 404:502-506(2000).  
-1- FUNCTION: NOR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubiquinol by a one-electron transfer pathway (By similarity).  
-1- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).  
-1- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).  
-1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).  
-1- SUBCELLULAR LOCATION: Inner membrane (Potential).  
-1- SIMILARITY: Belongs to the nqrF family.

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EMBL; AL152754; CAB84030.1; --  
PIR; D81918; D81918.  
HSSP; P23486; 1QFJ.  
HMAP; MF\_00430; -; 1.  
InterPro; IPR006058; 2Fe2S fd BS.  
InterPro; IPR008333; FAD binding\_6.  
InterPro; IPR001041; Ferredoxin\_6.  
InterPro; IPR001709; FPN\_cyt\_redtse.  
InterPro; IPR001433; Oxred\_FAD/NAD(P).  
Pfam; PF00970; FAD binding\_6; 1.  
Pfam; PF00111; fer2; 1.  
Pfam; PF00175; NAD binding\_1; 1.  
PRINTS; PR00371; FENCR.  
PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.  
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport; Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;  
KW Transmembrane; Inner membrane; Complete proteome.  
FT TRANSMEM 2 24 POTENTIAL.  
FT DOMAIN 34 114 FERREDOXIN.  
FT DOMAIN 270 387 CATALYTIC.  
FT METAL 67 67 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 73 73 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
FT METAL 108 108 IRON-SULFUR (2FE-2S) (BY SIMILARITY).  
SQ SEQUENCE 405 AA; 45165 MW; E22DC9CFB7B62B0A CRC64;

Query Match 16.8%; Score 104; DB 1; Length 405;  
Best Local Similarity 35.2%; Pred. No. 0.004;  
Matches 32; Conservative 14; Mismatches 41; Indels 4; Gaps 4;

QY 8 GTVTIAQTDRYACV-SGESILGMAKLGRRGIPVGLNGG-CGVCKVRVLRGAVRKLGP 65  
Db 32 GUITIKVNGEKLTPAGCKLLGALANEG-IFPSACGGSGCGCRVVKGGGDL-P 89

QY 66 ISRAHVSAAEENDGYALACRVDPDGDVELEV 96  
Db 90 TELSHISKREAREGCKRLSQVNVKTDMDIEV 120

RESULT 7

NORF NEIMA  
ID NORF NEIMA STANDARD; PRT; 405 AA.  
AC Q9K0M8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)





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DR InterPro: IPR001221; Phe_hydroxylase.
DR Pfam: PF00970; FAD_binding_6; 1.
DR Pfam: PF00111; fer2; 1.
DR Pfam: PF00175; NAD_binding_1; 1.
DR PRINTS: PR00406; CYTBSRDTASE.
DR PRINTS: PR00371; FENCR.
DR PRINTS: PR0410; PHEVDRLXASE.
DR PROSITE: PS00197; 2FE2S FERREDOXIN; 1.
DR Oxidoreductase; Monooxygenase; NADP; One-carbon metabolism;
KW Electron transport; Metal-binding; Iron-sulfur; Iron; 2Fe-2s;
KW Flavoprotein; FAD; 3D-structure.
FT METAL 42 42 IRON-SULFUR (2FE-2S).
FT METAL 47 47 IRON-SULFUR (2FE-2S).
FT METAL 50 50 IRON-SULFUR (2FE-2S).
FT METAL 82 82 IRON-SULFUR (2FE-2S).
FT NP BIND 221 235 FAD (NAD PART) (BY SIMILARITY).
SQ SEQUENCE 348 AA; 38541 MW; 7577BE408CA1C1F CRC64;

Query Match 16.2%; Score 100.5; DB 1; Length 348;
Best Local Similarity 30.0%; Pred. No. 0.0077;
Matches 30; Conservative 12; Mismatches 35; Indels 23; Gaps 5;

QY 9 TVTIAQTDE---RYACVSGSLLAGMAKLGRRGIPV--GCLNGCGVKVRVLRG----- 58
Db 6 TITAVTEGESLRECESDDEVITAAL---RQIFLMSSCREGGCATCALKCSGVDYDLK 62

QY 59 --AVRKLGPISRAHVSABEENDGYALACRVDPGDVELEV 96
Db 63 GCSVOALPP-----EEEGVLVLCRTYPTKTDLEIEL 94

RESULT 9
NORF PASMU STANDARD; PRT; 407 AA.
ID NORF PASMU STANDARD; PRT; 407 AA.
AC Q9CL6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na(+)-translocating NOR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F).
CN NORF OR PM1333.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI TaxID=747;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=PM70;
RC MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step
CC is catalyzed by nqrF, which accepts electrons from NADH and
CC reduces ubiquinone-1 to ubiquinol by a one-electron transfer
CC pathway (By similarity).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
CC ubiquinol + Na(+) (Out).
CC -!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
CC -!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
CC and nqrF (By similarity).
CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -!- SIMILARITY: Belongs to the nqrF family.

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CC EMBL: AB006171; AAK03417.1; -.
CC HSSP; P23486; IQFJ.
CC HAMAP; MF_00430; -, 1.
CC InterPro: IPR006058; 2Fe2S fd BS.
CC InterPro: IPR008333; FAD_binding_6.
CC InterPro: IPR001041; Ferredoxin.
CC InterPro: IPR001709; FPN cyt reductase.
CC InterPro: IPR001433; Oxid_FAD/NAD(P).
CC Pfam: PF00970; FAD_binding_6; 1.
CC Pfam: PF00111; fer2; 1.
CC Pfam: PF00175; NAD_binding_1; 1.
CC PRINTS: PR00371; FENCR.
CC PROSITE: PS00197; 2FE2S FERREDOXIN; FALSE NEG.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 5 24 POTENTIAL.
FT DOMAIN 34 116 FERREDOXIN.
FT DOMAIN 272 389 CATALYTIC.
FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 45252 MW; 9DAC403C9662C8C3 CRC64;

Query Match 16.2%; Score 100; DB 1; Length 407;
Best Local Similarity 32.6%; Pred. No. 0.01;
Matches 31; Conservative 16; Mismatches 38; Indels 10; Gaps 5;

QY 8 GTVTIAQTDRYACV---SGESLLAGMAKLGRRGIPV--GCLNGG-CGVKVRVLRGAVR 61
Db 32 GDITIEINDPSKAIHLPAAGKLLGALAS---QGIFVSSACGGGSCGQCIKVTGGGD 88

QY 62 KLGPISRAHVSABEENDGYALACRVDPGDVELEV 96
Db 89 IL-PTELSHISKREAGCYRLSCQVNVKNSMKVEL 122

RESULT 10
NORF VIBCH STANDARD; PRT; 408 AA.
ID NORF VIBCH STANDARD; PRT; 408 AA.
AC Q9X4Q8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na(+)-translocating NOR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F).
CN NORF OR VC2290.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI TaxID=666;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=El Tor N16961 / Serotype O1;
RC MEDLINE=99179036; PubMed=10077658;
RX Haese C.C., Mekalanos J.J.;
RA "Effects of changes in membrane sodium flux on virulence gene
RA expression in Vibrio cholerae.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3183-3187(1999).
RN [2] SEQUENCE FROM N.A.
RP STRAIN=El Tor N16961 / Serotype O1;
RC MEDLINE=20406833; PubMed=10952301;
RX Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.B., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

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RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RL cholerae.";
CC Nature 406:477-483 (2000).
CC -1- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step
CC is catalyzed by nqrF, which accepts electrons from NADH and
CC reduces ubiquinone-1 to ubiquinol by a one-electron transfer
CC pathway.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
CC ubiquinol + Na(+) (Out).
CC -1- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
CC -1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
CC and nqrF (By similarity).
CC -1- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -1- SIMILARITY: Belongs to the nqrF family.
CC
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CC
CC EMBL: AF117331; AAD29967.1; -.
CC EMBL: AE004300; AAF95434.1; -.
CC F1R; B82094; B82094.
CC HSSP; P33007; 1B9R.
CC TIGR; VC2290; -.
CC HAMAP; MF 00430; -.
CC InterPro; IPR006058; 2Fe2S fd BS.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001041; Ferredoxin.
CC InterPro; IPR001433; Oxred FAD/NAD(P).
CC Pfam; PF00970; FAD binding_6; 1.
CC Pfam; PF00111; fer2; 1.
CC Pfam; PF00175; NAD binding_1; 1.
CC PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE NEG.
CC Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 5 24 POTENTIAL.
FT DOMAIN 35 117 FERREDOXIN.
FT DOMAIN 273 390 CATALYTIC.
FT METAL 70 70 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 111 111 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 408 AA; 45066 MW; F5665E3623CAAD7B CRC64;

Query Match 16.0%; Score 99; DB 1; Length 408;
Best Local Similarity 34.4%; Pred. No. 0.013;
Matches 32; Conservative 14; Mismatches 41; Indels 6; Gaps 5;

QY 8 GTVTIA-QTDERYACVS--GESILAGMAKLRGRRIPVGCINGG-CGVCKVRVLRGAVRKL 63
DB 33 GDTITSINGDPEKAIVTQPGKKLLTALAGAG-VFVSSACGGGSGCQCRVKIKSGGGDIL 91
QY 64 GPISRAHVSABEENDGYALACRVDPGDVLEEV 96
DB 92 -PTDLHISKGEARGERLRACQVAVKADMDLEL 123

RESULT 11
DMPP PSESP
ID DMPP PSESP STANDARD; PRT; 352 AA.
AC P19734;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phenol hydroxylase P5 protein (EC 1.14.13.7) (Phenol 2-monooxygenase

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DE P5 component).
GN DMPP.
OS Pseudomonas sp. (strain CF600).
OG Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072230; PubMed=2254258;
RA Nordlund I., Powlowski J., Shingler V.;
RT "Complete nucleotide sequence and polypeptide analysis of
RT multicomponent phenol hydroxylase from Pseudomonas sp. strain
RT CF600.";
RL J. Bacteriol. 172:6826-6833 (1990).
RN [2]
RP PROBABLE FUNCTION, AND SEQUENCE OF 1-4.
RX MEDLINE=91072231; PubMed=2254259;
RA Powlowski J., Shingler V.;
RT "In vitro analysis of polypeptide requirements of multicomponent
RT phenol hydroxylase from Pseudomonas sp. strain CF600.";
RL J. Bacteriol. 172:6834-6840 (1990).
CC -1- FUNCTION: Catabolizes phenol, and some of its methylated
CC derivatives. P5 is required for growth on phenol, and for
CC in vitro phenol hydroxylase activity.
CC -1- FUNCTION: Probable electron transfer from NADPH, via FAD and the
CC 2Fe-2S center, to the oxygenase activity site of the enzyme.
CC -1- CATALYTIC ACTIVITY: Phenol + NADPH + O(2) = catechol + NADP(+) +
CC H(2)O.
CC -1- COFACTOR: P5 contains a FAD cofactor and a ferredoxin-type 2Fe-2S
CC cluster.
CC -1- PATHWAY: Phenol biodegradation; first step.
CC -1- SUBUNIT: The multicomponent enzyme phenol hydroxylase is formed
CC by P0, P1, P2, P3, P4 and P5 polypeptides.
CC -1- SIMILARITY: In the N-terminal section; belongs to the 2Fe2S plant-
CC type ferredoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M60276; AAA25944.1; -.
CC HSSP; P00235; 1FRR.
CC InterPro; IPR006058; 2Fe2S fd BS.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001041; Ferredoxin.
CC InterPro; IPR001433; Oxred FAD/NAD(P).
CC Pfam; PF00970; FAD binding_6; 1.
CC Pfam; PF00111; fer2; 1.
CC Pfam; PF00175; NAD binding_1; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PROSITE; PR00410; PHEHYDRKLASE.
CC PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
KW Flavoprotein; FAD; NADP; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Electron transport; Plasmid.
FT INIT MET 0 0
FT METAL 36 36 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 44 44 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 352 AA; 38346 MW; 1E8B7E6A6A3F12E4 CRC64;

Query Match 15.8%; Score 98; DB 1; Length 352;
Best Local Similarity 31.4%; Pred. No. 0.014;
Matches 27; Conservative 15; Mismatches 42; Indels 2; Gaps 2;

QY 10 VTIAQTDERYACVSGESILAGMAKLRGRRIPVGCINGGCGVKVRVLRGAVRKLGPISRA 69

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Db      4 VTTEPTGEVEVEDGQTILQAALRQG-VWLPFRACGHGTCTCKQVVEGEV-DIGREASP 61
QY      70 HVSAAEENDGYALACRVVPDGVLE 95
Db      62 ALMDIERDKVKLACCAIPLSLVIE 87

RESULT 12
NQRF VIBAL STANDARD; PRT; 407 AA.
AC Q56584;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na(+)-translocating NADH-quinone reductase subunit beta) (Na(+)-
DE translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F).
GN NQRF OR NQR6.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95246889; PubMed=7729558;
RA Hayashi M., Hirai K., Unemoto T.;
RT "Sequencing and the alignment of structural genes in the nqr operon
RT encoding the Na(+)-translocating NADH-quinone reductase from Vibrio
RL alginolyticus."; FEBS Lett. 363:75-77 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96230452; PubMed=8674603;
RA Tan K., Beattie P., Leach D.R.F., Rich P.R., Coulson A.F.W.,
RA Ward F.B.;
RT "Expression and analysis of the gene for the catalytic beta subunit of
RT the sodium-translocating NADH-ubiquinone oxidoreductase of Vibrio
RL alginolyticus."; Biochem. Soc. Trans. 24:123-125 (1996).
RN [3]
RP SEQUENCE OF 1-10.
RX MEDLINE=98149659; PubMed=9490015;
RA Nakayama Y., Hayashi M., Unemoto T.;
RT "Identification of six subunits constituting Na+-translocating NADH-
RT quinone reductase from the marine Vibrio alginolyticus.";
RL FEBS Lett. 422:240-242 (1998).
RN [4]
RP CHARACTERIZATION.
RC STRAIN=DSM 2171;
RX MEDLINE=98055703; PubMed=9395325;
RA Steuber J., Krebs W., Dimroth P.;
RT "The Na+-translocating NADH:ubiquinone oxidoreductase from Vibrio
RT alginolyticus -- redox states of the FAD prosthetic group and
RT mechanism of Ag+ inhibition.";
RL Eur. J. Biochem. 249:770-776 (1997).
RN [5]
RP INHIBITION OF ENZYMATIC ACTIVITY.
RA Unemoto T., Ogura T., Hayashi M.;
RT "Modifications by Na+ and K+, and the site of Ag+ inhibition in the
RT Na+-translocating NADH-quinone reductase from a marine Vibrio
RT alginolyticus."; Biochim. Biophys. Acta 1183:201-205 (1993).
RN [6]
RP INHIBITION OF ENZYMATIC ACTIVITY.
RX MEDLINE=20016049; PubMed=10549856;
RA Nakayama Y., Hayashi M., Yoshikawa K., Mochida K., Unemoto T.;
RT "Inhibitor studies of a new antibiotic, koromicin, 2-n-heptyl-4-
RT hydroxyquinoline N-oxide and Ag+ toward the Na+-translocating NADH-
RT quinone reductase from the marine Vibrio alginolyticus.";
RN Biol. Pharm. Bull. 22:1064-1067 (1999).
RN [7]

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RP REVIEW.
RX MEDLINE=21145117; PubMed=11248187;
RA Hayashi M., Nakayama Y., Unemoto T.;
RT "Recent progress in the Na(+)-translocating NADH-quinone reductase
RT from the marine Vibrio alginolyticus."; Biochim. Biophys. Acta 1505:37-44 (2001).
RN [8]
RP REVIEW.
RX MEDLINE=21145118; PubMed=11248188;
RA Steuber J.;
RT "Na(+)-translocation by bacterial NADH:quinone oxidoreductases: an
RT extension to the complex-I family of primary redox pumps."; Biochim. Biophys. Acta 1505:45-56 (2001).
RL CC -I- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step
CC is catalyzed by nqrF, which accepts electrons from NADH and
CC reduces ubiquinone-1 to ubiquinol by a one-electron transfer
CC pathway.
CC -I- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
CC ubiquinol + Na(+) (Out).
CC -I- COFACTOR: FAD and a 2Fe-2S cluster (Probable).
CC -I- ENZYME REGULATION: ACTIVATED BY NA(+) OR K(+). INHIBITED BY
CC SILVER.
CC -I- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
CC and nqrF.
CC -I- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -I- PTM: The N-terminus is blocked.
CC -I- SIMILARITY: Belongs to the nqrF family.
CC -----
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CC -----
CC EMBL; AB008030; BAA22915.1; -.
CC PUR; S65531; S65531.
CC HAMAP; MF_00430; -.
CC InterPro; IPR006058; 2Fe2S_fld_BS.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001041; Ferredoxin.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF00111; fer2; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC PRINTS; PR00371; FPNCR.
CC PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE NEG.
CC Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
CC Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
CC Transmembrane; Inner membrane.
CC TRANSMEM 5 24 POTENTIAL.
CC TRANSMEM 34 116 FERREDOXIN.
CC DOMAIN 272 389 CATALYTIC.
CC METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 45274 MW; A878E9DFCA87346 CRC64;

Query Match 15.8%; Score 98; DB 1; Length 407;
Best Local Similarity 31.2%; Pred. No. 0.016;
Matches 29; Conservative 17; Mismatches 41; Indels 6; Gaps 4;

QY 8 GTVTIAQTDERYACV---SSGLLAGMAKLGRRGIPVGLNGG-CGVCKVRVLRGAVKLL 63
Db 32 GDTITISVNDPFLAIVTPGGKLLSALAGAG-VFVSSACGGGCGCQCRVKVKGSGGDI 90
QY 64 GPISFAHVSAAEENDGYALACRVVPDGVLE 96

```

DR PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.  
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;  
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;

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DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR008333; FAD binding_6.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001433; Oxid FAD/NAD(P).
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT METAL 5 24 Potential.
FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 44945 MW; 1FDEC95F196715A2 CRC64;

Query Match 15.5%; Score 96; DB 1; Length 407;
Best Local Similarity 31.2%; Pred. No. 0.025; Indels 6; Gaps 4;
Matches 29; Conservative 16; Mismatches 42;

QY 8 GTVTI---QTDERYACVSGESLLAGMAKLGRRGIPVCGCLNGG-CGVCKVRLGAVRKL 63
Db 32 GDITVEINDEDEKSFAPAGDKLL---NMLSSHGIFVSSACGGGSCGQCRVTIKEGGD 88

QY 64 GPISRAHVSAREENDGYALACRVDPDGDVELEV 96
Db 91 -PTELDHITKGEAREGERLACQAVKMDMDEL 122

RESULT 15
NORF YERPE STANDARD; PRT; 407 AA.
ID NORF YERPE STANDARD; PRT; 407 AA.
AC Q8ZBZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na+)-translocating NOR subunit F (Na+)-NOR subunit F) (NOR complex
DE subunit F) (NOR-1 subunit F).
GN NORF OR YPO3235 OR Y0956.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RA "Genome sequence of Versinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Petherston J.D., Lindler L.P., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RA "Genome sequence of Versinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
CC -!- FUNCTION: NOR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step

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is catalyzed by nqrF, which accepts electrons from NADH and
reduces ubiquinone-1 to ubiquinol by a one-electron transfer
pathway (By similarity).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
ubiquinol + Na(+) (Out).
-!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
-!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
and nqrF (By similarity).
-!- SUBCELLULAR LOCATION: Inner membrane (Potential).
-!- SIMILARITY: Belongs to the nqrF family.

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EMBL; AJ414156; CAC92470.1; -.
EMBL; AE013698; AAM84537.1; -.
PIR; AB0393; AB0393.
HAWAP; MF_00430; -.
InterPro; IPR006058; 2Fe2S fd BS.
InterPro; IPR008333; FAD binding_6.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR001433; Oxid FAD/NAD(P).
Pfam; PF00970; FAD binding_6; 1.
Pfam; PF00111; fer2; 1.
Pfam; PF00175; NAD binding_1; 1.
PRINTS; PR00371; FENCR.
PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.
Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 2 24 POTENTIAL.
FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 45455 MW; 24AEFDA035483136 CRC64;

Query Match 15.0%; Score 93; DB 1; Length 407;
Best Local Similarity 30.5%; Pred. No. 0.05;
Matches 29; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

QY 8 GTVTI---AQTDERYACVSGESLLAGMAKLGRRGIPV--GCLNGG-CGVCKVRLGAVR 61
Db 32 GDITVEINDEDEKSFAPAGDKLL---NMLSSHGIFVSSACGGGSCGQCRVTIKEGGD 88

QY 62 KLGPISRAHVSAREENDGYALACRVDPDGDVELEV 96
Db 89 IL-PTELSHISKREAKEGCRACQNVVKNKIEL 122

Search completed: August 5, 2004, 13:16:03
Job time : 14 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 5, 2004, 13:13:04 ; Search time 38 Seconds  
(without alignments)  
979.767 Million cell updates/sec

Title: US-09-430-029-8  
Perfect score: 619

Sequence: 1 MDAGRCVGTWIAQTDERYA.....RLKPPFCGNACAGTAANK 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriaph:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	426	68.8	118	2	Q8VUT6	Q8vut6 burkholderi
2	365	59.0	113	2	Q9RB86	Q9rb86 burkholderi
3	365	59.0	123	2	Q9ZAN6	Q9zan6 comamonas s
4	361	58.3	119	2	Q9AE71	Q9ae71 pseudomonas
5	323	52.2	118	2	Q9S144	Q9s144 comamonas t
6	323	52.2	121	2	Q9ZNP1	Q9znp1 comamonas t
7	322	52.0	119	2	Q9Z418	Q9z418 pseudomonas
8	302	48.8	91	2	Q9EXM1	Q9exm1 escherichia s
9	286.5	46.3	109	2	Q9RB90	Q9rb90 burkholderi
10	267.5	43.2	111	2	Q93JX0	Q93jx0 pseudomonas
11	228.5	36.9	101	2	Q84964	Q84964 ralstonia s
12	217.5	35.1	115	2	Q9RAF3	Q9raf3 ralstonia s
13	205.5	33.2	112	2	Q9ANS9	Q9ans9 pseudomonas
14	203.5	32.9	119	2	Q45344	Q45344 burkholderi
15	189	30.5	105	2	Q847G8	Q847g8 pseudomonas
16	180.5	29.2	93	2	Q923W9	Q923w9 sphingomona

17	178	28.8	112	2	Q82817	Q82817 pseudomonas
18	175	28.3	112	2	Q53527	Q53527 pseudomonas
19	172.5	27.9	93	2	Q85974	Q85974 sphingomona
20	172.5	27.9	112	2	Q52061	Q52061 pseudomonas
21	170.5	27.5	100	2	Q8RQD9	Q8rqd9 pseudomonas
22	167.5	27.1	100	2	Q8KLVS	Q8klvs pseudomonas
23	166.5	26.9	101	2	Q52167	Q52167 pseudomonas
24	165.5	26.7	101	2	Q52176	Q52176 pseudomonas
25	163.5	26.4	112	2	Q24827	Q24827 acinetobact
26	144.5	23.3	342	2	Q53028	Q53028 rhodococcus
27	135.5	21.9	340	2	Q7WU95	Q7wu95 cycloclasti
28	134	21.6	349	16	Q8XWN9	Q8xwn9 ralstonia s
29	129.5	20.9	329	2	Q32476	Q32476 pseudomonas
30	129.5	20.9	329	2	Q82824	Q82824 pseudomonas
31	129.5	20.9	329	2	Q8GI14	Q8gi14 pseudomonas
32	125.5	20.3	329	2	Q84110	Q84110 janthinobac
33	123	19.9	346	2	Q85971	Q85971 sphingomona
34	120.5	19.5	336	16	Q7VSP1	Q7vsp1 bordetella
35	120	19.4	366	16	Q88A18	Q88a18 pseudomonas
36	119	19.2	353	2	Q84AQ0	Q84aq0 pseudomonas
37	118.5	19.1	336	16	Q7WEJ4	Q7wej4 bordetella
38	118.5	19.1	336	16	Q7W375	Q7w375 bordetella
39	117	18.9	368	16	Q88R18	Q88r18 pseudomonas
40	115	18.6	405	16	Q8E1D5	Q8e1d5 shewanella
41	114	18.4	337	16	Q8UG46	Q8ug46 agrobacteri
42	113	18.3	366	16	Q9HTF3	Q9htf3 pseudomonas
43	112.5	18.2	365	16	Q98CL3	Q98cl3 rhizobium l
44	111.5	18.0	360	2	Q9F3V4	Q9f3v4 pseudonocar
45	110	17.8	92	2	Q9XB57	Q9xb57 erwinia car

#### ALIGNMENTS

#### RESULT 1

Q8VUT6

ID Q8VUT6 PRELIMINARY; PRT; 118 AA.

AC Q8VUT6;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Ferredoxin-like protein PHKG.

GN PHKG.

OS Burkholderia kururiensis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI\_TaxID=89498;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang H., Luo H., Kanagata Y.;

RT "Involvement of a phenol hydroxylase of Burkholderia kururiensis KP23 in TCE degradation.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB063252; BAB79285.1; -.

DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006058; 2Fe2S fd BS.

DR InterPro; IPR001041; Ferredoxin.

DR Pfam; PF00111; fer2; 1.

DR PROSITE; PS00197; 2FE2S\_FERREDOXIN; 1.

KW Iron; iron-sulfur.

SQ SEQUENCE 118 AA; 12492 MW; 0F694FOEEROC4CF4 CRC64;

Query Match

Best Local Similarity 68.8%; Score 426; DB 2; Length 118;

Matches 80; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 1 MDAGRCVGTWIAQTDERYACVSGSLAGMAKLGRRGIPVGCCLNGGGCVKVRVLRGAV 60

Db 1 MNASEPKVAVTITQGEHYPCAVDESLLAGMARLGRGIPVGCCLNGGGCVKVRVLRGV 60

QY 61 RKLGPISRAHVSABEENDGYALACKRVDPGDVLEVAGRLRKPFFCGMAC 110

Db	61	RKLGPSRAHVSVEEEAGSYSLACRIAPQDVELEVAGKMQKPFRRGFAC	110
RESULT 2			
Q9RB86		PRELIMINARY;	PRT; 113 AA.
ID	Q9RB86		
AC	Q9RB86		
DT	01-MAY-2000	(TrEMBLrel. 13, Created)	
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Chloroplast-type ferredoxin.		
GN	PNT2		
OS	Burkholderia sp. RP007.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;		
OC	Burkholderiaceae; Burkholderia.		
OC	NCBI_TaxID=83784;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=RP007;		
RX	MEDLINE=99382283; PubMed=10448110;		
RA	Laurie A.D., Lloyd-Jones G.;		
RT	"Conserved and hybrid meta-cleavage operons from PAH-degrading		
RT	Burkholderia RP007.";		
RL	Biochem. Biophys. Res. Commun. 262:308-314(1999).		
CC	-1- COPACTOR; BINDS 1.2FE-2S CLUSTER (BY SIMILARITY).		
DR	EMBL; AF112137; AAF02429.1; -.		
DR	GO; GO:0005489; F:electron transporter activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR006058; 2Fe2S fd BS.		
DR	InterPro; IPR001041; Ferredoxin.		
DR	Pfam; PF00111; fer2; 1.		
DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.		
KW	Iron; Iron-sulfur.		
SQ	SEQUENCE 113 AA; 11991 MW; 3E7F77A539F77276 CRC64;		
Query Match 59.0%; Score 365; DB 2; Length 113;			
Best Local Similarity 67.0%; Pred. No. 4.2e-29;			
Matches 67; Conservative 14; Mismatches 19; Indels 0; Gaps 0;			
Qy	10	VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRGAVRKLGPIISRA	69
Db	12	VTVKQTGERFSCALGESLLAGMARLGRGIPVGLCLSGCGVCKVACVCGSVRKIGAMGRT	71
Qy	70	HVSAEEENDGYALACRVVPGDVELEVAGRLRKPFPCGMA	109
Db	72	HISEVEEAQGVVACRVAPTDDELEVGVGMQKPFKGLS	111
RESULT 3			
Q9ZAN6		PRELIMINARY;	PRT; 123 AA.
ID	Q9ZAN6		
AC	Q9ZAN6		
DT	01-MAY-1999	(TrEMBLrel. 10, Created)	
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Ferredoxin.		
GN	CDOT.		
OS	Comamonas sp. JS765.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;		
OC	Comamonadaceae; Comamonas.		
OC	NCBI_TaxID=58226;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=JS765;		
RX	MEDLINE=98113817; PubMed=9451836;		
RA	Parales R.E., Ontl T.A., Gibson D.T.;		
RT	"Cloning and sequence analysis of a catechol 2,3-dioxygenase gene from		
RT	the nitrobenzene-degrading strain Comamonas sp JS765.";		
RL	J. Ind. Microbiol. Biotechnol. 19:385-391(1997)		
CC	-1- COPACTOR; BINDS 1.2FE-2S CLUSTER (BY SIMILARITY).		
DR	EMBL; U93030; AAC79917.1; -.		
DR	GO; GO:0005489; F:electron transporter activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
RESULT 4			
Q9AE71		PRELIMINARY;	PRT; 119 AA.
ID	Q9AE71		
AC	Q9AE71;		
DT	01-JUN-2001	(TrEMBLrel. 17, Created)	
DT	01-OCT-2001	(TrEMBLrel. 18, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Plant-type ferredoxin.		
GN	TDND1.		
OS	Pseudomonas putida.		
OG	Plasmid pTDN1.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
OC	NCBI_TaxID=303;		
RN	[1]		
RP	SEQUENCE OF 1-29 FROM N.A.		
RA	Fukumori F., Saint C.P.;		
RT	"Aniline degradation in Pseudomonas putida UCC22(pTDN1): Initial		
RT	characterization of its conversion to catechol.";		
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE OF 1-29 FROM N.A.		
RX	MEDLINE=97144524; PubMed=8990291;		
RA	Fukumori F., Saint C.P.;		
RT	"Nucleotide sequences and regulational analysis of genes involved in		
RT	conversion of aniline to catechol in Pseudomonas putida UCC22		
RT	(pTDN1).";		
RL	J. Bacteriol. 179:399-408(1997).		
DR	EMBL; D85415; BAB62044.1; -.		
DR	GO; GO:0046821; C:extrachromosomal DNA; IEA.		
DR	GO; GO:0005489; F:electron transporter activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR006058; 2Fe2S fd BS.		
DR	InterPro; IPR001041; Ferredoxin.		
DR	Pfam; PF00111; fer2; 1.		
DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.		
KW	Iron; Iron-sulfur; Plasmid.		
SQ	SEQUENCE 119 AA; 12227 MW; 1CDD536BA2C431CE CRC64;		
Query Match 58.3%; Score 361; DB 2; Length 119;			
Best Local Similarity 63.2%; Pred. No. 1.1e-28;			
Matches 74; Conservative 9; Mismatches 26; Indels 8; Gaps 2;			
Qy	1	MDAGRVCG--TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRG	58
Db	1	MQATVAVGPSSVCVVVQTGTACSPGESLLRGLRGLRGKIPVGCNGGCGVCKVRVIRG	60
Qy	59	AVRKLGPIISRAHVSAAEENDGYALACRVVPGDVELEVAGRLRKPFPCGMA	115
Db	61	CVRALGPVSRHVSAAEENDGYALACRVVPGDVELEVAGRLRKPFPCGMA	111
RESULT 5			
Query Match 59.0%; Score 365; DB 2; Length 113;			
Best Local Similarity 67.0%; Pred. No. 4.2e-29;			
Matches 67; Conservative 14; Mismatches 19; Indels 0; Gaps 0;			
Qy	10	VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRGAVRKLGPIISRA	69
Db	12	VTVKQTGERFSCALGESLLAGMARLGRGIPVGLCLSGCGVCKVACVCGSVRKIGAMGRT	71
Qy	70	HVSAEEENDGYALACRVVPGDVELEVAGRLRKPFPCGMA	109
Db	72	HISEVEEAQGVVACRVAPTDDELEVGVGMQKPFKGLS	111



DR Pfam: PF00111; fer2; 1.  
DR PROSITE; PS00197; 2FE2S\_FERREDOXIN; 1.  
KW Iron; Iron-sulfur.  
SQ SEQUENCE 121 AA; 12722 MW; C29F512A8BDCC749 CRC64;  
Query Match 52.2%; Score 323; DB 2; Length 121;  
Best Local Similarity 64.6%; Pred. No. 7.4e-25;  
Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;  
QY 10 VTTAQTDERYACVSGESLLAGMAKLGRRGIPVCLNGCGVCKVRLRGAVRKLGPISRA 69  
Db 9 VSVETQGTDTYACGTHTSLLSGMLRLGRKGIPIVGVNGGCGVCKVRLRGAVRKLGPISRA 68  
QY 70 HVSAAEENDGYALACRVVDPGDVELEVAGRLRKPFF 105  
Db 69 HVSDDLDDQGYTLACRVAPLEAVRIAVRQRLHKPFF 104  
RESULT 7  
Q9Z418 PRELIMINARY; PRT; 119 AA.  
ID Q9Z418  
AC Q9Z418;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Ferredoxin.  
GN CBZT.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GU31;  
RX MEDLINE=99138753; PubMed=9973359;  
RA Mars A.E., Kingma J., Kaschabek S.R., Reineke W., Janssen D.B.;  
RT "Conversion of 3-chlorocatechol by various catechol 2,3-dioxygenases  
RT and sequence analysis of the chlorocatechol dioxygenase region of  
RT Pseudomonas putida GU31.";  
RL J. Bacteriol. 181:1309-1318(1999).  
CC -1- COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).  
DR EMBL; AF109307; AAD05249.1; -;  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR006058; 2Fe2S fd BS.  
DR Pfam; PF00111; fer2; 1.  
DR PROSITE; PS00197; 2FE2S\_FERREDOXIN; 1.  
KW Iron; Iron-sulfur.  
SQ SEQUENCE 119 AA; 12747 MW; 12256BE66062FF06 CRC64;  
Query Match 52.0%; Score 322; DB 2; Length 119;  
Best Local Similarity 56.4%; Pred. No. 9.4e-25;  
Matches 62; Conservative 13; Mismatches 35; Indels 0; Gaps 0;  
QY 9 TTTAQTDERYACVSGESLLAGMAKLGRRGIPVCLNGCGVCKVRLRGAVRKLGPISR 68  
Db 10 SVHVMGTGETTFPCATDESLLQGMRLGRKGIPIVGVNGGCGVCKVRLRGAVRKLGPISR 69  
QY 69 AHVSAEENDGYALACRVVDPGDVELEVAGRLRKPFFCGMACAGTAANK 118  
Db 70 AHVSAEAEARGTILACRVAPVTPVQLEVVGVGFEKVFSGFVSSTNEINK 119  
RESULT 8  
Q9EXM1 PRELIMINARY; PRT; 91 AA.  
ID Q9EXM1  
AC Q9EXM1;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Chloroplast-type ferredoxin.  
GN ALND.



[illegible]

Search completed: August 5, 2004, 13:16:54  
Job time : 40 secs